

STIC-Biotech/ChemLib

119873

From: Shukla, Ram
Sent: Tuesday, April 20, 2004 4:41 PM
To: STIC-Biotech/ChemLib
Subject: 10/055,106

Please provide sequence search for:

SEQ ID NO 1
Nucleic acid encoding SEQ ID NO 2
12mer Oligosearch

Thanks.

Ram R. Shukla, Ph.D.

Primary Examiner
AU 1632
2D29 Remsen Bldg
Mailbox 2C18
Phone: (571) 272-0735
Fax: (571) 273-0735

RECEIVED
APR 20 2004
STIC

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 4/26
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

DB 995 CACCTTCATTTTACACAATGAACCTTGTGATTCTGTCTTAGAATGAGAAG 1054
QY 267 GluIlePheLeuSerValThrAlaIleSer-----CysTyrAspLeuLeuPhe 283
DB 1055 TCCGTGGTCATAAACCTTCTCTGTGCTGCATCCAATTGTTGTTGACCTCTCTATAT 1114
QY 284 ValPheGlyGlySerHisTyrPheLysGln 293
DB 1115 TTCTTTTCTGGGGTAACTTTTAGGAAAAGG 1144

Search completed: April 25, 2004, 22:24:44
Job time : 488 secs

US-10-055-106C-2 (1-305) x US-10-400-991-7 (1-1358)

Alignment Scores:
Pred No.: 1, 1e-11 Length: 1358
Score: 250.00 Matches: 68
Percent Similarity: 48.71% Conservative: 83
Best Local Similarity: 21.94% Mismatches: 131
Query Match: 15.70% Indels: 28
DB: 13 Gaps: 11

US-10-055-106C-2 (1-305) x US-10-400-991-7 (1-1358)

QY 3 GlyHisAsnThrSerArgAsnSerSerCys-----AspProIleValThrPro 18
DB 242 GGAATCTGACAGTATCTTCGCCACATGCCATGACACTATTGATGACTTCGCAATCAA 301
QY 19 HisLeuIleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIle 38
DB 302 GTGATTCCACCTTGATCTATGATCTCTGTTAGCTTCTTTGGCAATGGCTTGTTG 361
QY 39 LeuPheLeuLeuValLys---MetAsnThrArgSerValThrThrMetAlaValIleAsn 57
DB 362 CTCATGTCTCTCAATAAACCTATCACAAAGAGTCAGCCTTCCAAAGTATACATGATTAAT 421
QY 58 LeuValValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIle 77
DB 422 TTACAGTAGCAGACTTACTTTGTGTGTCACACACTGCTCTCCGTGGTCTATTATGTT 481
QY 78 LysLys---ThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
DB 482 CACAAAGGCATTTGGCTCTTTGGTGACTTCTTTGGCGCCTCAGCACCTATGCTTTGTAT 541
QY 97 IleHisMetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIle 116
DB 542 GTCACCTCTATTGTAGCATCTTCTTATGACAGCC-----ATGAGC 583
QY 117 PhePheLysCys-----LysAspLysValGluPheTyrArgLysLeu 130
DB 584 TTTTTCGGTGCATTCGCAATGTTTTCAGTCCAGAACATTAATTTGGTTACACAGAAA 643
QY 131 HisAlaValAlaAlaSerAlaGlyMetTrpThrLeuValIleValIleValProLeu 150
DB 644 AAGCCAGGTTGTGTGTAGTATTTGGATTTTGGATTTTGACATTTTGACCACTCTCCATT 703
QY 151 ValValSerArgTyrGlyIleHisGluGluTyrAsnGluHisCysPheLysPheHis 170
DB 704 CTAATGGCCAAA---CCACAAAAGATGAGAAAATAATACCAAGTGTCTTTGAGCCCCCA 760
QY 171 LysGlu---LeuAlaTyrThrTyrValLysIleIleAsnTyr-----MetIleValIle 187
DB 761 CAAGCAATCAAACTAAATAATCTTTTGGTCTGTGATTAATGTCATGTTGTTGTTGGC 820
QY 188 PheValIleAlaValAlaValIleLeuLeuValPheGlnValPheIleIleMetLeuMet 207
DB 821 TTTATCATCCCTTTTGGTTATTATAATTGCTGTTACACAATGATCAATTTGACCTTACTA 880
QY 208 ValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTyrAlaGlnLeuLysAsn 227
DB 881 AAAAAATCAATGAAAAAATCTGTCAAGTCAATATAAAGGCTATAGGAATGATC----- 934
QY 228 LeuPhePheIleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIleTyr 247
DB 935 ATGGTCGTGACCGCTGCTTTTGTAGTCTTTCAGCTATCATATTCATCAACGTACCAT 994
QY 248 TyrLeuAsnValVal---ThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsn 266

QY 120 slyAspLysValGluPheTyrArgLysLeuHisAlaVal 133
 Db 42 CAAAGCAAGTGGATTCTACAGAAACTGCATGCTGTG 3

RESULT 14

US-10-290-078-20
 ; Sequence 20, Application US/10290078
 ; Publication No. US20030124596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carroll, Joseph A.
 ; TITLE OF INVENTION: Methods and Compositions for Treating
 ; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
 ; FILE REFERENCE: 14395, 14618, 17692 or 58874
 ; CURRENT APPLICATION NUMBER: US/10/290,078
 ; CURRENT FILING DATE: 2002-11-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 1014
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1014)
 ; US-10-290-078-20

Alignment Scores:
 Pred. No.: 7,44e-12 Length: 1014
 Score: 250.00 Matches: 68
 Percent Similarity: 48.71% Conservative: 83
 Best Local Similarity: 21.94% Mismatches: 131
 Query Match: 15.70% Indels: 28
 DB: 15 Gaps: 11

US-10-055-106c-2 (1-305) x US-10-290-078-20 (1-1014)

QY 3 GlyHisAsnThrSerArgAsnSerGys-----AppProIleValThrPro 18
 Db 13 GGAATCTCAGCATGATCTCTCCACATGCCACATGACATATTGATGACTCCGCAATCAA 72
 QY 19 HisLeuIleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIle 38
 Db 73 GTGATTCCACTTGACTCTATGATCTGTGTAGGCTCTTGGCAATGGCTTTGTG 132
 QY 39 LeuPheLeuLeuValLys---MetAsnThrArgSerValThrMetAlaValIleAsn 57
 Db 133 CTCTATGCTCTCATAAAAACCTATCACAGAAGTCCAGCTTCCAAAGTATACATGATTAAT 192
 QY 58 LeuValValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIle 77
 Db 193 TTACAGTAGCAGATCTACTTTGTGTGTCACATGCTCTCCGTGGTCTATATGTT 252
 QY 78 LysLys---ThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
 Db 253 CACAAGGCAATTGGCTCTTTGGTGAATCTTTGTGCGCCCTCAGCAGCCTCTTGTAT 312
 QY 97 IleHisMetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIle 116
 Db 313 GTCACCTCTATTGTAGCATCTCTTTATGACAGCC-----ATAGC 354
 QY 117 PhePheLysCys-----LysAspLysValGluPheTyrArgLysLeu 130
 Db 355 TTTTTCGGTGTGATTCGAATTTTCCAGTCCAGACATTAATTTGGTTACACAGAA 414
 QY 131 HisAlaValAlaAsnAlaGlyMetTrpThrLeuValIleValIleValValProLeu 150
 Db 415 AAGCCAGGTTGTGTGTAGTATTGGATTTTGGATTTTGACCATCTCTCCATT 474
 QY 151 ValValSerArgTyrGlyIleHisGluGluTyrAsnGluGluHisCysPhePheHis 170
 Db 475 CTAATGGCCAAA---CCACAAAAGATGAGAAAATAATACCAAGTGTCTTTGACGCCCA 531

QY 171 LysGlu---LeuAlaTyrThrTyrValLysIleIleAsnTyr-----MetIleValIle 187
 Db 532 CAAAGCAACTCAAACTAAATAATCATGTTTGGTCTTGCAATTATGTCAATGTTGTTGGC 591
 QY 188 PheValIleAlaValAlaValIleLeuValGlnValPheIleIleMetLeuMet 207
 Db 592 TTATCATCCCTTTTGTATTATATATCTGTGTACACAATGATCATTTTGCCTTACTA 651
 QY 208 ValGlnLysLeuArgHisSerLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsn 227
 Db 652 AAAAAATCAATGAAAAAATCTGCAAGTCATAAAAAAGGCTATAGNATGATC----- 705
 QY 228 LeuPhePheIleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIleTyr 247
 Db 706 ATGTCGTGACCGCTGCTCTTTTGTAGTCTTTCATGTCATATCATATTTCAACGTACCAT 765
 QY 248 TyrLeuAsnValVal---ThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsn 266
 Db 766 CACCTTCATTTTACACAATGAAACTAAACCTGTGATCTCTTGTAGNATCAGAG 825
 QY 267 GluIlePheLeuSerValThrAlaIleSer-----CysTyrAspLeuLeuLeuPhe 283
 Db 826 TCGTGTGTCATAACCTTGTCTCTGCTGCAATCCAAATTTGCTTGTACCTCTCTCTAT 885
 QY 284 ValPheGlyGlySerHisTrpPheLysGln 293
 Db 886 TTCCTTCTGGGGTAACTTTAGGAAAGG 915

RESULT 15

US-10-400-991-7
 ; Sequence 7, Application US/10400991
 ; Publication No. US20030224417A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Glucksmann, Maria A.
 ; APPLICANT: Weich, Nadine S.
 ; APPLICANT: Hunter, John J.
 ; APPLICANT: White, David
 ; APPLICANT: MacBeth, Kyle J.
 ; APPLICANT: Williamson, Mark J.
 ; APPLICANT: Meyers, Rachel E.
 ; APPLICANT: Chun, Miyoung
 ; TITLE OF INVENTION: 14400, 2838, 14618, 15334, 14274, 32164,
 ; TITLE OF INVENTION: 39404, 38911, 26904, 31237, 18057, 18405, 32705, 23224,
 ; TITLE OF INVENTION: 27423, 32700, 32712 AND 12216, NOVEL SEVEN-TRANSMEMBRANE
 ; TITLE OF INVENTION: PROTEINS/G-PROTEIN COUPLES RECEPTORS
 ; FILE REFERENCE: MPI03-0240NMIM
 ; CURRENT APPLICATION NUMBER: US/10/400,991
 ; CURRENT FILING DATE: 2003-03-27
 ; PRIOR APPLICATION NUMBER: US 10/190,469
 ; PRIOR FILING DATE: 2002-07-05
 ; PRIOR APPLICATION NUMBER: US 09/439,159
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: US 09/137,063
 ; PRIOR FILING DATE: 1998-08-20
 ; PRIOR APPLICATION NUMBER: US 10/167,192
 ; PRIOR FILING DATE: 2002-06-11
 ; PRIOR APPLICATION NUMBER: US 09/420,187
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: US 09/173,869
 ; PRIOR FILING DATE: 1998-10-16
 ; PRIOR APPLICATION NUMBER: US 10/339,056
 ; PRIOR FILING DATE: 2003-01-09
 ; PRIOR APPLICATION NUMBER: US 09/377,429
 ; PRIOR FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: US 09/136,726
 ; PRIOR FILING DATE: 1998-08-19
 ; PRIOR APPLICATION NUMBER: US 09/911,583
 ; PRIOR FILING DATE: 2001-07-24
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: FastSeq for Windows Version 4.0

```
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-366-504-1

Alignment Scores:
Pred. No.: 2,896-87 Length: 810
Score: 1141.00 Matches: 219
Percent Similarity: 89.55% Conservative: 21
Best Local Similarity: 81.72% Mismatches: 28
Query Match: 71.67% Indels: 0
DB: 0 Gaps: 0

US-10-055-106C-2 (1-305) x US-10-366-504-1 (1-810)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
Db 1 ATGGATGGATATAATACCTCTGAGAAATCTCTGTGACCCCTATATGTCACACCACTTA 60
QY 21 IleSerLeuTyrPheIleValIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 61 ACATCGATTACTTCTAGTGTCTGAGGAGCTGTGGAGGCTCATCTCCATCCCTGTTTC 120
QY 41 LeuLeuValIysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 121 TTCTGGTGAATGAACCTCACTGAGTGCAGTGCACCACTGCTGTATCAACCTCGTGGTG 180
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrIleLeuIleLysThr 80
Db 181 GTTCATGGGTCTTCTCTACTGACGGTGCCTTTCGCTTGCATACCTCATCAAGGAGCT 240
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 241 TGAACGTTGATATACCTCTCGCAATTTGTGAGTGCCATGTATACATATCCACATGTAC 300
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleLeuPhePheLysCys 120
Db 301 CTCACGTTCTCTTCTACGTGGTGATAGTACTAGTATCATCAGATACCTCATCTTCAAGCGT 360
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyr 140
Db 361 AGAGCAAGATAGATTTCTATAGAAATTCATGACGTTGCTGCAAGTTCGCGCATGTGG 420
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 421 CTTCCTGGTGTATGTTATTTGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 480
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
Db 481 TACAATGAGCAACAGTCTTTAGATTCATTAAGAACTTGCCATGATGCTGTGCGAGTT 540
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 541 ATCAACTATATATAGTATGTTGTGTATAGTGTGTGCTGTGCTGTGCTGTGCTGTGCT 600
QY 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 601 GTCTTCATCATGTTCCATGGTGGGAGTTTGCACCTCTTACTATCCACACAGAG 660
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 661 TTCTGGGCACACACTGAAAATCTTTCTTTATAGGTATCATTTATTTGTTTCTTCCC 720
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260
Db 721 TACCAGTCTCTCAGGATTTATTTACTTGTATGTTGTGGCACCATCCCAAGAGCTGAAAAC 780
QY 261 LysValAlaPheTyrAsnGluIle 268
Db 781 AAGTTGCAATTTTACATGAATC 804

RESULT 13
US-09-782-974C-21/c
```

```
; Sequence 21, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 41USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-974C-21
```

```
Alignment Scores:
Pred. No.: 3,77e-48 Length: 447
Score: 674.00 Matches: 133
Percent Similarity: 92.25% Conservative: 0
Best Local Similarity: 92.25% Mismatches: 0
Query Match: 42.34% Indels: 1
DB: 10 Gaps: 0
```

US-10-055-106C-2 (1-305) x US-09-782-974C-21 (1-447)

```
QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
Db 402 ATGCTGCGCAATATACCTCTGAGAAATTCCTTTCGCGATCTCTAGTGACACCCACTTA 343
QY 21 IleSerLeuTyrPheIleValIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 342 ATCAGCCTCTACTTCTATAGTCTTATTGCGGCGCTGTGGTGTCTATTTCCATTTCTTTC 283
QY 41 LeuLeuValIysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 282 CTCCTCGTGAATAATGAACACCCGCGTCACTGACCCCATCGCGGTCAATTAATCTTGGTGTG 223
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrIleLeuLysLysThr 80
Db 222 GTCCACAGCGTTTCTCTGACAGTGCAATTCGTTGACCTACTCATCAAGAGACT 163
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 162 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCATGCTGCATCCACATGTGTAC 103
QY 101 LeuThr-PheLeuPheTyrValIleLeuValThrArgTyrIleLeuPheLysCys 120
Db 102 CTCACGGTTCTTCTTCTATGTTGTTGATCTGTTGTCACAGATACCTCATCTTCTTCAAGTG 43
```

Db 565 ATCACTATATGATAGTCACTTTTGTGTCATAGCGGTTGCTGTGATTCCTGTGCTTCCAG 624
Qy 201 ValPheileleuMetLeuValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 625 GTCTTCATCATATGTTGATGTGTCAGAGAGCTACGCCACTCTTTACTATCCACAGGAG 684
Qy 221 PheTrpAlaGlnLeuLysLeuPhePheileleGlyValleuValCysPheLeuPro 240
Db 685 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTCATCCTGTGTTTCTTCC 744
Qy 241 TyrGlnPhePheArgileTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 745 TACCAATTTCTTAGGATCTATCTACTTGAATTTGTGACGCAATTCATGCCCTGTAGCAGC 804
Qy 261 LysValAlaPheTyrAsnGlnLilePheLeuSerValThrAlaileSerCysTyrAspLeu 280
Db 805 AAGTTGTCATTTTATAACGAAATCTTCTTGAGTGTAAACGCAATTAGCTGTCTATGATTG 864
Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysatleileGlyLeuTrpAsn 300
Db 865 CTTCCTCTTTGTCTTTGGGGAGCCATTTGTTTAAACAAAGATAATTGCTTATGGAAT 924
Qy 301 CysValLeuCysArg 305
Db 925 TGTGTTTTGTGCCGT 939

RESULT 11

US-10-085-233B-1
; Sequence 1, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870. A HUMAN G-PROTEIN COUPLED
; FILE OF INVENTION: RECEPTOR AND USES THEREFOR
; FILE REFERENCE: MEI2001-021P1RCP1M
; CURRENT APPLICATION NUMBER: US/10/085,233B
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/272,677
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (147)...(1085)
; OTHER INFORMATION: n at position 1384 can be any
; OTHER INFORMATION: nucleotide
US-10-085-233B-1

Alignment Scores:

Pred. No.:	158e-124	Length:	1684
Score:	1587.00	Matches:	304
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.67%	Mismatches:	0
Query Match:	99.69%	Indels:	0
DB:	15	Gaps:	0

US-10-055-106c-2 (1-305) x US-10-085-233B-1 (1-1684)

Qy 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProileValThrProHisLeu 20
Db 171 ATGCTTGGCCACATACCTCCAGAAATTCCTCTTGGGATCCTATAGTACACCCCACTTA 230
Qy 21 IleSerLeuTyrPheileValleuileGlyLeuValGlyValleuSerileLeuPhe 40
Db 231 ATCAGCCTCTACTTCATAGTGTCTATTGGCGGCTGGTGGGTCTATTTCATTTCTTTC 290
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValleuAsnLeuValVal 60
Db 291 CTCTCGTGAAATGAACACCCCGTCAGTGACCAACCATGCGGTCTTAATTAATGGTGGTG 350

Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrIleuileLysLysThr 80
Db 351 GTCCACAGCGTTTTTCTGCTGACAGTGCCATTTGCTTGACCTACCTACCTCATCAAGAGACT 410
Qy 81 TrpMetPheGlyLeuProPheCysLeuPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 411 TGGATGTTTGGGCTGCCCTTCTGCATAATTTGTGAGTGCCATGCTGCACTCCACATGTAC 470
Qy 101 LeuThrPheLeuPheTyrValValleuLeuValThrArgTyrIleuilePhePheLysCys 120
Db 471 CTCAGTTCTCTATTCTATGTTGTCATCTCTGTGTCACAGATACCTCATCTTCTTCAAGTGC 530
Qy 121 LysAspLysValGlnPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrp 140
Db 531 AAAGACAAAGTGGAAATCTACAGAAACTGTCATGCTGTGCTGCCAGTGTGGCATTTGG 590
Qy 141 ThrLeuValleuValleuValProLeuValValSerArgTyrGlyIleHisGlnGlu 160
Db 591 ACGTGTGTGATTGTCATTTGTTACCCCTGCTGCTCCCGGTATGGAATCCATGAGAA 650
Qy 161 TyrAsnGlnGluHisCysPhePheHisLysGlnLeuAlaTyrThrTyrValLysIle 180
Db 651 TACAATGAGGAGCAGCTGTTTAAATTTTACAAAGAGCTTGTTCACACATATGTGAAATC 710
Qy 181 IleAsnTyrMetIleValleuPheValleuAlaValAlaValleuLeuValPheGln 200
Db 711 ATCACTATATGATAGTCACTTTTGTGTCAGCCGTTGCTGTGATTCCTGTGCTTCCAG 770
Qy 201 ValPheileleuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 771 GTCTTCATCATATGTTGATGTCAGAGCTACGCCACTCTTTACTATATCCACAGGAG 830
Qy 221 PheTrpAlaGlnLeuLysAsnLeuPhePheileGlyValleuValCysPheLeuPro 240
Db 831 TCTGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTTGTGTTTCTTCTTCCC 890
Qy 241 TyrGlnPhePheArgileTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 891 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCATGCTGTAGCAGC 950
Qy 261 LysValAlaPheTyrAsnGlnLilePheLeuSerValThrAlaileSerCysTyrAspLeu 280
Db 951 AAGTTGCAATTTATAACGAAATCTTCTTGAGTGTAAACAGCAATTAGCTTATGGAAT 1010
Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleileGlyLeuTrpAsn 300
Db 1011 CTTCCTCTTGTCTTTGGGGAGCCATTTGTTTAAACAAAGATAATTGCTTATGGAAT 1070
Qy 301 CysValLeuCysArg 305
Db 1071 TGTGTTTTGTGCCGT 1085

RESULT 12

US-10-366-504-1
; Sequence 1, Application US/10366504
; Publication No. US20030166008A1
; GENERAL INFORMATION:
; APPLICANT: Bishindirelo, Haifeng
; APPLICANT: Dressler, Holly
; APPLICANT: Cai, Jidong
; APPLICANT: Wright, Paul
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND USES TH
; FILE REFERENCE: USAV2002/0002 USNP
; CURRENT APPLICATION NUMBER: US/10/366,504
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 60/356,686
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: GB 0219574.1
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1

Alignment Scores:		1.58e-122	Length:	113306
Pred. No.:		1592.00	Matches:	305
Score:		100.00%	Conservative:	0
Percent Similarity:		100.00%	Mismatches:	0
Best Local Similarity:		100.00%	Indels:	0
Query Match:		16	Gaps:	0
DB:				
US-10-055-106C-2 (1-305) x US-10-292-798-1007 (1-113306)				
QY	1	MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu	20	
DB	11540	ATGCCTGGCCACATACCTCCAGGAATTCCTCTGGATCTCTATAGTACACCCCACTTA	11599	
QY	21	IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe	40	
DB	11600	ATCAGCCTCTACTTCATAGTGCCTATTGGCGGGCTGGTGGTGTCAATTCATTCCTTTTC	11659	
QY	41	LeuLeuValIysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuVal	60	
DB	11660	CTCTGTGTGAATGAACACCCGGTCAAGTACCCACCATGGCGGTCAATTAATTCCTGGTG	11719	
QY	61	ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrIleuIleLysThr	80	
DB	11720	GTCCACAGCGTTTCTGCTGACAGTGCCTATTCGCTTGACCTACCTCATCAAGAGACT	11779	
QY	81	TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr	100	
DB	11780	TGGATGTTGGGCTGGCTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC	11839	
QY	101	LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleuIlePheLysCys	120	
DB	11840	CTCAGTTCCTATTCTATGTGTGTGATCTGTCACAGATACCTCATCTTCCTCAAGTGC	11899	
QY	121	LysAspIysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr	140	
DB	11900	AAACACAAAGTGAATCTACAGAAACTGCATGCTGTGGTGCATGTGGCATGTGG	11959	
QY	141	ThrLeuValIleValIleValIleValProLeuValValSerArgTyrGlyIleHisGlu	160	
DB	11960	ACGTGTGTGATGTCAATGTGTGATCCCTGCTGCTCCGGTATGGAATCCATGAGAA	12019	
QY	161	TyrAsnGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValIysIle	180	
DB	12020	TACAAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGCTTACACATATGTGAATC	12079	
QY	181	IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln	200	
DB	12080	ATCAACTATATGATAGTCAATTTTGTATAGCCGTGTGTGTGATTCCTGTTCCTCAG	12139	
QY	201	ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu	220	
DB	12140	GTCTTCATCATATGATGTGATGGTGAGAGTACGCCACTCTTTTACTATCCACAGAG	12199	
QY	221	PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro	240	
DB	12200	TTCTGGGCTCAGCTGAAAACTATTTTATAGGGGTCACTCTGTTGTTTCTCTCCC	12259	
QY	241	TyrGlnPhePheArgIleTyrTyrIleuAsnValThrHisSerAsnAlaCysAsnSer	260	
DB	12260	TACCAGTTCCTTAGGATCTATTACTTGAATGTGTGACGCATTCGAATGCTGTAAACAGC	12319	
QY	261	LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu	280	
DB	12320	AAGGTGTGATTTTATACGAATCTCTTGTAGTGTACAGCAATTAGCTGTATGATTG	12379	
QY	281	LeuLeuPheValPheGlyCysHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn	300	
DB	12380	CTTCTCTTGTCTTGGGGAGCCATTCGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT	12439	
QY	301	CysValLeuCysArg	305	
DB	12440	TGTGTTTGTGCGGT	12454	

```

; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 2525
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-782-974C-81

Alignment Scores:
Pred. No.: 1,02e-124 Length: 2525
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DS: 10 Gaps: 0

US-10-055-106c-2 (1-305) x US-09-782-974C-81 (1-2525)

QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 27 ATGCCTGGCCACAAATACCTCCAGGATTCCTCTGGGATCCTATAGTGACACCCCACTTA 86
QY 21 IleSerLeuThrPheIleValIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 87 ATCAGCCTCTACTTCTATAGTGTCTATTTGGGGGCTGGTGGTGTCTATTTCTTCTTTC 146
QY 41 LeuLeuValIysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 147 CTCTGTGTGAATGAAACACCCCGTCAGTGACACCACTGGCGGTCTATTAACCTGGTGG 206
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrThrIleLeuIleLysThr 80
Db 207 GTCCACAGCGCTTTTCTGTCTGACAGTGCCATTTTCGCTTGACCTACCTCATCAAGAGACT 266
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 267 TGAATGTTGGGTGGCTCTCTGCAATTTGTGAGTGCCATGTGTCACATCCACATGTAC 326
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleLeuPhePheLysCys 120
Db 327 CTCACGTTCTCTTCTATGTGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 386
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyr 140
Db 387 AAAGACAAAGTGAATTTCTACAGAAACTCATGCTGTGCTGCCAGTGTGCTGCTGCTGCTG 446
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 447 ACGTGTGTGATTTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 506
QY 161 TyrAsnGluGluHisCysPheLysPheHisGlyLeuLeuAlaTyrThrTyrValLysIle 180
Db 507 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTCTCTTACACATATGTGAATTC 566

; ILeAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
; 567 ATCACTATATATAGTATGATTTTGTGATAGCCGTTGCTGTGATTTCTGTGTGCTTCCAG 626
; 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
; 627 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTTACTATATCCACAGGAG 686
; 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
; 687 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTGTTTCTTCCC 746
; 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
; 747 TACCAGTTCITTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTGTAAACAG 806
; 261 LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
; 807 AAGGTTGCAATTTTATACGAAATCTTCTGAGTGTAAACAGCAATAGCTGCTATGATTG 866
; 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
; 867 CTCTCTTCTTGTCTTGGGGAGGCAATGGTTTAAAGCAAAAGATAATTGCTTATGGAAT 926
; 301 CysValLeuCysArg 305
; 927 TGTGTTTGTGCCGT 941

RESULT 9
US-10-292-798-1007
; Sequence 1007, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1007
; LENGTH: 113306
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: source
; LOCATION: (1) .. (113306)
; FEATURE: (1) .. (113306)
; NAME/KEY: CDS
; LOCATION: (201) .. (207)
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (11526) .. (12452)
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (37954) .. (38097)
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (98732) .. (98784)
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (112891) .. (113106)
; US-10-292-798-1007
```

QY	181	IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln	200
Db	541	ATCAACTATATAGTACATATTTTGTGTAGCCGTTGCTGTGATCTGTGTCTTCACG	600
QY	201	ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuSerHisGlnGlu	220
Db	601	GTCTTCATCATTTAGTTGATGGTGAGAGAGCTACGCCACTCTTTACTATCCACAGGAG	660
QY	221	PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro	240
Db	661	TTCTGGGCTCAGCTGAAAAACCATTTTATAGGGGTCTATCTGTGTTCCTTCCCTCC	720
QY	241	TyrGlnPhePheArgIleTyrTyrLeuAsnValIleThrHisSerAsnAlaCysAsnSer	260
Db	721	TACCACTCTTTAGGATCATTTACTTGAATGTTGTGACCATTCATGCTGTATGATTTG	780
QY	261	LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu	280
Db	781	AAGGTTGCATTTTATAACGAAATCTTCTGAGTGTAAACAGCAATTAGCTGTATGATTTG	840
QY	281	LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn	300
Db	841	CTTCTCTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAGATAATTGGCTTATGGAAT	900
QY	301	CysValLeuCysArg	305
Db	901	TGTGTTTGTGCCGT	915
RESULT 7			
US-10-017-161-1193			
; Sequence 1193, Application US/10017161			
; Publication No. US20030143668A1			
; GENERAL INFORMATION:			
; APPLICANT: SUWA, MAKIKO			
; APPLICANT: ASAI, KIYOSHI			
; APPLICANT: AKIYAMA, YUTAKA			
; APPLICANT: ABEURATANI, HIROYUKI			
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS			
; FILE REFERENCE: 084335/0152			
; CURRENT APPLICATION NUMBER: US/10/017,161			
; CURRENT FILING DATE: 2002-12-18			
; PRIOR APPLICATION NUMBER: JP 2001/246789			
; PRIOR FILING DATE: 2001-06-18			
; NUMBER OF SEQ ID NOS: 2430			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1193			
; LENGTH: 1318			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: source			
; LOCATION: (1)..(1318)			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (201)..(1118)			
US-10-017-161-1193			
Alignment Scores:			
Pred. No.:	4.32e-125	Length:	1318
Score:	1592.00	Matches:	305
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0
US-10-055-106C-2 (1-305) x US-10-017-161-1193 (1-1318)			
QY	1	MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu	20
Db	201	ATGCTGGCCACATACCTCCAGGAATTCCTCTTGGCATCTCATAGTGACACCCCACTTA	260
QY	21	IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe	40

Db	261	ATCAGCCTCTACCTCATAGTGTCTATTGGCGGCTGTGGTGTCTATTTCCATCTTTTC	320
QY	41	LeuLeuValLysVetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal	60
Db	321	CTCTGTGTGAAATGAACACCCGCTAGTGACCAACCATGSCGGTCATTAACTTGGTGGTG	380
QY	61	ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr	80
Db	381	GTCCACAGCGTTTTTCTGTGTGACAGTGCCATTTCCGTTGACCTACCTCATCAAGAAGACT	440
QY	81	TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr	100
Db	441	TGSAATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC	500
QY	101	LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys	120
Db	501	CTCAGCTTCCTATTTCTATGTGGTGATCTCTGTGCACACAGATACCTCATCTCTTCAAGTGC	560
QY	121	LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaIleSerAlaGlyMetTrp	140
Db	561	AAAGACAAAGTGAATTTCTACAGAAAACTGCATGCTGTGGCTGCCAGTGTGGCATGTGG	620
QY	141	ThrLeuValIleValIleValValProLeuValValSerArgTyrGlyIleHisGluGlu	160
Db	621	ACGCTGGTGAATGTTCATTTGTGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA	680
QY	161	TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle	180
Db	681	TACAATGAGGAGCAGCTGTTTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAATC	740
QY	181	IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln	200
Db	741	ATCAACTATATAGTAGTACATTTTTTGTGTATAGCCGTTGCTGTGATCTCTGTGTCTTCAG	800
QY	201	ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu	220
Db	801	GTCTTCATCATTTATGTTGATGCTGCAGAAAGCTAGCCCACTCTTTACTATCCACAGGAG	860
QY	221	PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro	240
Db	861	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGTCATCTCTTGTGTCTTCTTCCC	920
QY	241	TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer	260
Db	921	TACCACTCTTTAGGATCTATTTACTTGAATGTTGTGACCATTCCAATGCCTGTAAACAGC	980
QY	261	LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu	280
Db	981	AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAAACAGCAATTAGCTGTATGATTTG	1040
QY	281	LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn	300
Db	1041	CTTCTCTTGTCTTTGGGGAGGACCATTTGGTTAAGCAAAAGATAATTGGCTTATGGAAT	1100
QY	301	CysValLeuCysArg	305
Db	1101	TGTGTTTGTGCCGT	1115

RESULT 8
US-09-782-974C-81
; Sequence 81, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human TGR343
US-10-188-405-9

Alignment Scores:
Pred. No.: 2,68e-125 Length: 918
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-055-106C-2 (1-305) x US-10-188-405-9 (1-918)

QY 1 MetProGlyHisAenThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
DB 1 ATGCCTGGCCCAATACCTCCAGGAATTCCTTTCGGATCCTATAGTGACACCCCACTTA 60
QY 21 IleSerLeuTyrPheIleValValleuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 61 ATCAGCCTCTACTTCATAGTGTCTTATTCGGGGCTGGTGGGTGCATTTCCATCTTTTC 120
QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
DB 121 CTCCTGGTGAAATGAAACACCCGGTCAGTGACCACTGGGGTGCATTAACCTTGGTGTG 180
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
DB 181 GTCCACAGCGTTTCTCTGTGACAGTGGCCATTTCCGCTTGACCTACCTCATCAAGAAGACT 240
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
DB 241 TGGATGTTTGGGCTGCGCTCTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300
QY 101 LeuThrPheLeuPheTyrValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
DB 301 CTCACGTTCTATTCATGTGTGATCCCGGTGATCCAGATACCTCATCTTCTCAAGTGC 360
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140
DB 361 AAAGCAAAAGTGGATTCACAGAAACATGCGTGTGGCTGCCAGTGGCTGGCAATGTGG 420
QY 141 ThrLeuValIleValIleValProLeuValLysArgTyrClyIleHisGluGlu 160
DB 421 AGCTGGTGATTCATCTGTGTACCCCGTGTCTCCCGGTATGGAATCCATGAGAA 480
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
DB 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 540
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
DB 541 ATCAACTATATAGTCAATTTTGTATAGCGGTGTGTGTATCTGTGTGTCTTCCAG 600
QY 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
DB 601 GTCTTCATCATATGTTGTGTGAGAGAGTACGCCACTCTTTACTATCCCAAGAGGAG 660
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
DB 661 TTCGGGCTCAGCTGAAACCACTATTTTATAGGGGTGCATCTTGTGTGTCTTCCCTCC 720
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260
DB 721 TACCAGTCTCTTAGGATCTATTACTTGAATGTTGTGACGCATTTCCAAATGCCGTGAACAGC 780
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
DB 781 AAGGTGTCATTTTATACGAAATCTTCTTGAGGTGTAACAGCAATTAAGTGTGATGATTTG 840
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleLeuGlyLeuTrpAsn 300

DB 841 CTTCTCTTTGTCTTTGGGGAAGCCATTGGTTTAAGCAAGATAATATTGGCTTATGGAAT 900
QY 301 CysValLeuCysArg 305
DB 901 TGTGTTTTGTGGGT 915
RESULT 6
US-10-293-171-1
; Sequence 1, Application US/102931171
; Publication No. US20030138418A1
; GENERAL INFORMATION:
; APPLICANT: Eishingdrelo, Haifeng
; APPLICANT: Cai, Jidong
; APPLICANT: Gassenhuber, Johann
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND USES TH
; FILE REFERENCE: USAV2001/0158 US NP
; CURRENT APPLICATION NUMBER: US/10/293,171
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US60/354,150
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-293-171-1

Alignment Scores:
Pred. No.: 3,16e-125 Length: 1040
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-055-106C-2 (1-305) x US-10-293-171-1 (1-1040)

QY 1 MetProGlyHisAenThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
DB 1 ATGCCTGGCCCAATACCTCCAGGAATTCCTTTCGGATCCTATAGTGACACCCCACTTA 60
QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 61 ATCAGCCTCTACTTCATAGTGTCTTATTCGGGGCTGGTGGGTGCATTTCCATCTTTTC 120
QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
DB 121 CTCCTGGTGAAATGAAACACCCGGTCAGTGACCACTGGCGGTGCATTAACCTTGGTGTG 180
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
DB 181 GTCCACAGCGTTTCTCTGTGACAGTGGCCATTTCCGCTTGACCTACCTCATCAAGAAGACT 240
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
DB 241 TGGATGTTTGGGCTGCGCTCTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
DB 301 CTCAGTTCCTTATTCATGTGTGATCCTGGTGCACAGATACCTCATCTTCTTCAAGTGC 360
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140
DB 361 AAAGCAAAAGTGGATTCACAGAAACATGCGTGTGGCTGCCAGTGGCTGGCATGTGG 420
QY 141 ThrLeuValIleValIleValProLeuValLysArgTyrGlyIleHisGluGlu 160
DB 421 ACGTGTGATTTGATTTGTTGCTACCCCTGGTGTCTCTCCGGTATGGAATCCATGAGAA 480
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
DB 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 540


```

Db      541 ATCACTATATAGTCAATTTTGTATAGCGTTCCTGATCTGCTGCTTCACG 600
Qy      201 ValPheIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db      601 GTCTTCATCATATGTTGATGTGAGAAAGCTACGCCACTCTTTACTATCCACACGAG 660
Qy      221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db      661 TTCCTGGGCTCAGTGAACCACTATTTTATAGGGGTCACTCTGTTGTTGTTTCCTCC 720
Qy      241 TyrGlnPhePheArgIleTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260
Db      721 TACCACTCTTTAGGATCTATTACTTTGAATGTGTGACGCAATTCGAATGCCGTGAACAGC 780
Qy      261 LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db      781 AGGTTGCAATTTTATACGAAATCTTCTTGAGTGAACGAATTAGCTGCTATGATTG 840
Qy      281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
Db      841 CTTCTCTTTGCTTTGGGGAGACCATTTGTTTAAAGCAAGATATTCGCTTATGGAAT 900
Qy      301 CysValLeuCysArg 305
Db      901 TGTGTTTGTGCCGT 915

RESULT 4
US-10-055-106C-1
; Sequence 1, Application US/10055106C
; Publication No. US20030017536A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Harland, Lee
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PC10970AGLK
; CURRENT APPLICATION NUMBER: US/10/055,106C
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: GB0101739.1
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/267,341
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-055-106C-1

Alignment Scores:
Pred. No.:      2,68e-125      Length:      918
Score:          1592.00      Matches:      305
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              13          Gaps:      0

US-10-055-106C-2 (1-305) x US-10-055-106C-1 (1-918)
Qy      1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db      1 ATGCTGGCCCAATACCTCCAGGAATTCCTCTGCGATCTATAGTACACCCCACTTA 60
Qy      21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db      61 ATCAGCCTCTACTTCATAGTCTTATTGGCGGCTGGTGGTGTCAATTCATTTCTTTTC 120
Qy      41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
Db      121 CTCCTGGTGAATAATGAACCCCGTCAGTACCCACCATGGCGGTCAATTAATTCGTGGTG 180
Qy      61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80

```

```

Db      181 GTCCACAGCCGTTTTCTGTGACAGTGCCATTTCTGCTTGACCTACCTCATCAAGAGACT 240
Qy      81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db      241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTATC 300
Qy      101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db      301 CTCACGTTCTTATCTATGTTGGTATCCTGCTCACAGATACCTCATCTTCTTCAAGTGC 360
Qy      121 LysAspLysValGlnPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrp 140
Db      361 AAAGCAAAAGTGAATTTCTACAGAAACTGCATGCTGTGCTGCCAGTGTGCGATGTGG 420
Qy      141 ThrLeuValIleValIleValValProLeuValValSerArgTyrGlyIleHisGlnGlu 160
Db      421 ACGTGTGTGATTGTCAATTTGTGGTACCCCTGTTGTCTCCCGTATGGATCCATGAGAA 480
Qy      161 TyrAsnGlnGluHisCysPheLysPheHisLysGlnLeuAlaTyrThrTyrValLysIle 180
Db      481 TACATGAGGAGCACTGTTTAAATTTCAAAAGAGCTGCTTACACATATGTGAAATC 540
Qy      181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
Db      541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATTCCTGTGCTTTCAG 600
Qy      201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db      601 GTCTTCATCATATGTTGATGTGTCAGAGAGCTACGCCACTCTTTACTATCCACAGAG 660
Qy      221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db      661 TTCCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTCACTCTGTTGTTGTTCTCTCCC 720
Qy      241 TyrGlnPhePheArgIleTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260
Db      721 TACCAGTCTTTTAGATCTATTAATGATGTTGTGACGCAATTCGAATCCATGCTATGATTG 780
Qy      261 LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db      781 AAGGTTGCAATTTTATACGAAATCTTCTTGAGTGAACAGCAATTAGCTGCTATGATTG 840
Qy      281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
Db      841 CTTCTCTTTGCTTTGGGGAGACCATTTGTTTAAAGCAAGATATTCGCTTATGGAAT 900
Qy      301 CysValLeuCysArg 305
Db      901 TGTGTTTGTGCCGT 915

RESULT 5
US-10-188-405-9
; Sequence 9, Application US/10188405
; Publication No. US20030082585A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Dai, Kang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Zhao, Jiagang
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030082585A1:el Receptors
; FILE REFERENCE: 018781-008410US
; CURRENT APPLICATION NUMBER: US/10/188,405
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 918
; TYPE: DNA

```


Pred. No.: 2.68e-125 Length: 918
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-055-106C-2 (1-305) x US-09-995-225-3 (1-918)

```
QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
DB 1 ATGCTGGCCCAATACCTCCAGGAATTCCTTGGATCCTATAGTGACACCCCACTTA 60
QY 21 IleSerLeuTyPheIleValleuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 61 ATCAGCCTCTATTCATAGTCTTATTTGGCGGGTGGTGGTGTCACTTCCATCTTTTC 120
QY 41 LeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
DB 121 CTCCTGGTGAANAATGAACCCGGTCAGTGACCACTGGCGGTCACTTAAGTGGTGG 180
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyLeuIleLysLeuThr 80
DB 181 GTCCACAGCGATTTCTCTGACAGTGCCATTTGCTTGACCTACCTACCTCAACAGAGACT 240
QY 81 TrpMetPheGlyLeuProPheCysIlePheValSerAlaValMetLeuHisIleHisMetTy 100
DB 241 TGGATGTTTGGGCTGGCCCTTCTGAAATTTGTGAGTGCCATGCTGCACATCCATGTAC 300
QY 101 LeuThrPheLeuPheTyValIleLeuValThrArgTyLeuIlePhePheLysCys 120
DB 301 CTCAGTTTCCTATTCATAGTGGTATCTGCTGACCAAGAGCTGCTTACATATGTGAAATC 360
QY 121 LysAspIleValGluPheTyArgIleHisAlaValAlaAlaSerAlaGlyMetTrp 140
DB 361 AAAGACAAAGTGGAAATCTACAGAAATCTGATGCTGCTGGCTGCAGTGTGGCATGTGG 420
QY 141 ThrLeuValIleValIleValIleValProLeuValValSerArgTyGlyIleHisGluGlu 160
DB 421 ACGCTGGTGATTTGATTTGATGTTGATGTTGTTCTCCCGGTATGGAATCCATGAGAA 480
QY 161 TyrAsnGluHisCysPhePhePheHisIleGluLeuAlaTyThrTyValLysIle 180
DB 481 TACAATGAGGAGCACTGTTTAAATTTTACAAAGAGCTGCTTACACATATGTGAAATC 540
QY 181 IleAsnTyMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
DB 541 ATCACTATATGATAGTATTTTGTATAGCCGTTGCTGTGATCTGTGGTCTTCCAG 600
QY 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
DB 601 GTCTTTCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
DB 661 TTCTGGGCTACGCTGAAACCACTATTTTATAGGGGTATCTTGTGTTGTTTCCCTCC 720
QY 241 TyrGlnPhePheArgIleTyTyLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
DB 721 TACCAGTTCTTTAGGATCTATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 261 LysValAlaPheTyAsnGluIlePheLeuSerValThrAlaIleSerCysTyAspLeu 280
DB 781 AAGGTTGCAATTTTAAACGAAATCTTCTGAGTGTAAACGAAATAGCTGTATGATTTG 840
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnIleIleGlyLeuTrpAsn 300
DB 841 CTCTCTTTTGTCTTTGGGGGAGCACTTGGTTTAAAGCAAAAGATAATGGCTTATGGAAT 900
QY 301 CysValLeuCysArg 305
DB 901 TGTCTTTTGTGCCGT 915
```

RESULT 3

US-10-297-908A-2
; Sequence 2, Application US/10297908A
; Publication No. US20040029793A1
; GENERAL INFORMATION:
; APPLICANT: MORIYA, Takeo
; APPLICANT: ITO, Takahashi
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: MIYAJIMA, No. US20040029793A1
; TITLE OF INVENTION: No. US20040029793A1 G Protein-Coupled Receptor Protein and its
; FILE REFERENCE: 2737 USOP
; CURRENT APPLICATION NUMBER: US/10/297,908A
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: PCT/JP01/05061
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: JP 2000-184596
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: JP 2000-223887
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Human
US-10-297-908A-2

Alignment Scores:
Pred. No.: 2.68e-125 Length: 918
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-055-106C-2 (1-305) x US-10-297-908A-2 (1-918)

```
QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
DB 1 ATGCTGGCCCAATACCTCCAGGAATTCCTTGGATCCTATAGTGACACCCCACTTA 60
QY 21 IleSerLeuTyPheIleValleuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 61 ATCAGCCTCTATTCATAGTCTTATTTGGCGGGTGGTGGTGTCACTTCCATCTTTTC 120
QY 41 LeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
DB 121 CTCCTGGTGAANAATGAACCCGGTCAGTGACCACTGGCGGTCACTTAAGTGGTGG 180
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyLeuIleLysLeuThr 80
DB 181 GTCCACAGCGATTTCTCTGACAGTGCCATTTGCTTGACCTACCTACCTCAACAGAGACT 240
QY 81 TrpMetPheGlyLeuProPheCysIlePheValSerAlaMetLeuHisIleHisMetTy 100
DB 241 TGGATGTTTGGGCTGGCCCTTCTGAAATTTGTGAGTGCCATGCTGCACATCCATGTAC 300
QY 101 LeuThrPheLeuPheTyValIleLeuValThrArgTyLeuIlePhePheLysCys 120
DB 301 CTCAGTTTCCTATTCATAGTGGTATCTGCTGACCAAGAGCTGCTTACATATGTGAAATC 360
QY 121 LysAspIleValGluPheTyArgIleHisAlaValAlaAlaSerAlaGlyMetTrp 140
DB 361 AAAGACAAAGTGGAAATCTACAGAAATCTGATGCTGCTGGCTGCAGTGTGGCATGTGG 420
QY 141 ThrLeuValIleValIleValIleValProLeuValValSerArgTyGlyIleHisGluGlu 160
DB 421 ACGCTGGTGATTTGATTTGATGTTGATGTTGTTCTCCCGGTATGGAATCCATGAGAA 480
QY 161 TyrAsnGluHisCysPhePhePheHisIleGluLeuAlaTyThrTyValLysIle 180
DB 481 TACAATGAGGAGCACTGTTTAAATTTTACAAAGAGCTGCTTACACATATGTGAAATC 540
QY 181 IleAsnTyMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
```

;; PRIOR APPLICATION NUMBER: 60/270,286
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,355
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/270,266
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,032
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,358
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,356
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/290,917
;; PRIOR FILING DATE: 2001-05-14
;; PRIOR APPLICATION NUMBER: 60/309,208
;; PRIOR FILING DATE: 2001-07-31
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 918
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-995-225-3

Alignment Scores:
Pred. No.: 2.68e-125 Length: 918
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-055-106C-2 (1-305) x US-09-995-225-3 (1-918)

Qy 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 1 ATGCCTGGCCACATACTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60
Qy 21 ILeSerLeuTyrPheIleValLeuIleGlyValGlyValGlyValIleSerIleLeuPhe 40
Db 61 ATCAGCCTCTACTTCATAGTGCCTTATTTGGGGCTGGTGGTGGTGCATTTCCATTTCTTC 120
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 121 CTCTGTGTGAATGAACACCCGGTCACTGACCCACCATGCGGTCAATTAACCTGGTGGTG 180
Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrIleuIleLysLysThr 80
Db 181 GTCCACAGCGCTTTTCTGCTGACAGTGCCTATTTGGCTTGACCTACCTCATCAAGAAAGACT 240
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 241 TGGATGTTGGCTGCCCTCTCGCAATTTGTGAGTGCCATGTGCACATCCACATGTAC 300
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleuLeuPhePheLysCys 120
Db 301 CTCACGTTCTCTATCTATGTGGTATCCTGGTACCAGATACCTCATCTCTTCAAGTGC 360
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrp 140
Db 361 AAGACAAATGGAAATCTACAGAAACTGCATGCTGTGCTGCCAGTGTGCATGTGG 420
Qy 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 421 ACGTGTGTATGTCAATGTGTACCCCTGTGTCTCCCGGTATGGAATCCATGAGAA 480
Qy 161 TyrAsnGluHisCysPheLysPheHisGlyLeuAlaTyrThrTyrValLysIle 180
Db 481 TACAATGAGGAGCACTGTTTAAATTTCAAGAGCTTCTTACACATATGGAATC 540
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 541 ATCAACTATATAGTATCAATTTTGTGATAGCCGTTGCTGTGATTTCTGTTGGTCTTCCAG 600

Qy 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 601 GTCCTTCATCATATATGTTGTCGAGGAGCTAGCCACTCTTTACTATCCACAGAG 660
Qy 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTGTTGTTCTTCCC 720
Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 721 TACCAGTCTCTTAGGATCTATTTACTTGAATGTTGACGCATTTCAATGCTGTAAACAGC 780
Qy 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 781 AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGTATGATTG 840
Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleGlyLeuTrpAsn 300
Db 841 CTTCTCTTTGCTTTGGGGGAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Qy 301 CysValLeuCysArg 305
Db 901 TGTGTTTGTGCCGT 915

RESULT 2

US-09-995-225-3
; Sequence 3, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPELLANT: Chu, Zhi Liang
; APPELLANT: Dang, Huong T.
; APPELLANT: Lowitz, Kevin P.
; APPELLANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
; FILE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-225-3

Alignment Scores:

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 25, 2004, 19:58:35 ; Search time 469 Seconds
(without alignments)
2932.049 Million cell updates/sec

Title: US-10-055-106c-2
Perfect score: 1592
Sequence: 1 MPGHNTSRNSSCDPIVPHL.....GGSHWFQKIKGLMNCVLCR 305

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+ -p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US10055106/runat_21042004_161132_26226/app_query.fasta_1.455
-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40 cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODS=LOCAL -OUTFMT=pcr -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10055106 @CGN 1 1 221 @runat_21042004_161132_26226
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOC=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=120 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

ALIGNMENTS

RESULT 1

US-09-995-225-3
; Sequence 3, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AEN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12

1	1592	100.0	918	9	US-09-995-225-3	Sequence 3, Appli
2	1592	100.0	918	10	US-09-995-225-3	Sequence 3, Appli
3	1592	100.0	918	13	US-10-297-908A-2	Sequence 1, Appli
4	1592	100.0	918	13	US-10-055-106C-1	Sequence 9, Appli
5	1592	100.0	918	15	US-10-188-405-9	Sequence 1, Appli
6	1592	100.0	1040	15	US-10-293-171-1	Sequence 1193, Ap
7	1592	100.0	1318	15	US-10-017-161-1193	Sequence 81, Appl
8	1592	100.0	2525	10	US-09-782-974C-81	Sequence 107, Ap
9	1592	100.0	113306	16	US-10-292-798-1007	Sequence 3, Appli
10	1587	99.7	939	15	US-10-085-233B-3	Sequence 1, Appli
11	1587	99.7	1684	15	US-10-085-233B-1	Sequence 1, Appli
12	1141	71.7	810	15	US-10-366-504-1	Sequence 21, Appl
13	674	42.3	447	10	US-09-782-974C-21	Sequence 20, Appl
14	250	15.7	1014	15	US-10-290-078-20	Sequence 7, Appli
15	250	15.7	1358	13	US-10-400-991-7	Sequence 4, Appli
16	250	15.7	1358	15	US-10-167-192-4	Sequence 19, Appl
17	250	15.7	1359	15	US-10-290-078-19	Sequence 546, App
18	247	14.5	1014	15	US-10-225-567A-546	Sequence 9, Appli
19	231.5	14.5	1077	9	US-09-826-508-9	Sequence 413, App
20	231.5	14.5	1146	15	US-10-225-567A-413	Sequence 417, App
21	231.5	14.5	1402	15	US-10-225-567A-417	Sequence 363, App
22	231.5	14.5	1402	16	US-10-295-027-363	Sequence 1038, Ap
23	231.5	14.5	1480	16	US-10-295-027-1038	Sequence 38, Appl
24	231.5	14.5	1481	14	US-10-071-766-136	Sequence 136, App
25	231.5	14.5	1481	15	US-10-101-510-627	Sequence 627, App
26	231.5	14.5	1481	15	US-10-101-510-633	Sequence 633, App
27	231.5	14.5	1489	10	US-09-741-783-2	Sequence 2, Appli
28	231.5	14.5	1489	13	US-10-165-844-2	Sequence 881, App
29	231.5	14.5	1489	13	US-10-276-774-881	Sequence 21, Appl
30	231	14.5	1444	9	US-09-919-172-21	Sequence 85, Appl
31	231	14.5	1444	9	US-09-974-298-85	Sequence 87, Appl
32	231	14.5	1444	15	US-10-121-101B-2	Sequence 1, Appli
33	231	14.5	1041	15	US-10-321-807-87	Sequence 54, Appl
34	228	14.3	1041	9	US-09-826-791-1	Sequence 54, Appl
35	225	14.1	1026	10	US-09-991-225-54	Sequence 5, Appli
36	225	14.1	1026	13	US-10-369-405-54	Sequence 6, Appli
37	225	14.1	1039	17	US-10-182-605-1	Sequence 1, Appli
38	225	14.1	1041	9	US-09-826-791-5	Sequence 29, Appl
39	225	14.1	1041	9	US-09-866-230-6	Sequence 57, Appl
40	225	14.1	1041	10	US-09-828-478-1	Sequence 29, Appl
41	225	14.1	1041	10	US-09-591-225-29	Sequence 21, Appl
42	225	14.1	1041	13	US-10-343-650A-57	Sequence 29, Appl
43	225	14.1	1041	13	US-10-369-405-29	Sequence 1, Appli
44	225	14.1	1041	13	US-10-349-021-1	
45	225	14.1	1041	13	US-10-349-021-1	

Query Match 3.1%; Score 28; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.0006;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 419 GGACCGTGGTGCATTGCTGTTGTTACC 446
 Db 28 GGACCGTGGTGCATTGCTGTTGTTACC 1

Search completed: April 25, 2004, 20:06:18
 Job time : 462 secs

;; PRIOR FILING DATE: 1998-10-13
;; PRIOR APPLICATION NUMBER: 60/253,404
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/255,366
;; PRIOR FILING DATE: 2000-12-12
;; PRIOR APPLICATION NUMBER: 60/270,286
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,365
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/270,266
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,032
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,358
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,356
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/290,917
;; PRIOR FILING DATE: 2001-05-14
;; PRIOR APPLICATION NUMBER: 60/309,208
;; PRIOR FILING DATE: 2001-07-31
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 26
;; LENGTH: 29
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: No. US20020193584A1 Sequence
US-09-995-225-26

Query Match 3.2%; Score 29; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 GCTGCACATCCACATGTACTCAGTTCC 310
Db 29 GCTGCACATCCACATGTACTCAGTTCC 1

RESULT 14
US-09-995-225-26/c
;; Sequence 26, Application US/09995225
;; Publication No. US20030139588A9
;; GENERAL INFORMATION:
;; APPLICANT: Chen, Ruoping
;; APPLICANT: Chu, Zhi Liang
;; APPLICANT: Dang, Huong T.
;; APPLICANT: Lowitz, Kevin P.
;; APPLICANT: Pride, Cameron
;; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
;; FILE REFERENCE: AREN-0308
;; CURRENT FILING DATE: 2001-11-26
;; PRIOR FILING DATE: 2001-11-26
;; PRIOR APPLICATION NUMBER: 60/253,404
;; PRIOR FILING DATE: 1998-10-13
;; PRIOR APPLICATION NUMBER: PCT/US99/23938
;; PRIOR FILING DATE: 1998-10-13
;; PRIOR APPLICATION NUMBER: 60/253,404
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/255,366
;; PRIOR FILING DATE: 2000-12-12
;; PRIOR APPLICATION NUMBER: 60/270,286
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,365
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/270,266
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,032
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,358
;; PRIOR FILING DATE: 2001-04-06

;; PRIOR APPLICATION NUMBER: 60/282,356
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/290,917
;; PRIOR FILING DATE: 2001-05-14
;; PRIOR APPLICATION NUMBER: 60/309,208
;; PRIOR FILING DATE: 2001-07-31
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 26
;; LENGTH: 29
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-26

Query Match 3.2%; Score 29; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 GCTGCACATCCACATGTACTCAGTTCC 310
Db 29 GCTGCACATCCACATGTACTCAGTTCC 1

RESULT 15
US-09-995-225-25/c
;; Sequence 25, Application US/09995225
;; Publication No. US20020193584A1
;; GENERAL INFORMATION:
;; APPLICANT: Chen, Ruoping
;; APPLICANT: Chu, Zhi Liang
;; APPLICANT: Dang, Huong T.
;; APPLICANT: Lowitz, Kevin P.
;; APPLICANT: Pride, Cameron
;; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
;; FILE REFERENCE: AREN-0308
;; CURRENT FILING DATE: 2001-11-26
;; PRIOR FILING DATE: 2001-11-26
;; PRIOR APPLICATION NUMBER: 60/253,404
;; PRIOR FILING DATE: 1998-10-13
;; PRIOR APPLICATION NUMBER: PCT/US99/23938
;; PRIOR FILING DATE: 1998-10-13
;; PRIOR APPLICATION NUMBER: 60/253,404
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/255,366
;; PRIOR FILING DATE: 2000-12-12
;; PRIOR APPLICATION NUMBER: 60/270,286
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,365
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/270,266
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,032
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,358
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,356
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/290,917
;; PRIOR FILING DATE: 2001-05-14
;; PRIOR APPLICATION NUMBER: 60/309,208
;; PRIOR FILING DATE: 2001-07-31
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: Patentin version 3.1
;; SEQ ID NO 25
;; LENGTH: 28
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-25

121 CTCCTGGTGAATGAACACACCCGGTCAGTGAACCAACCATGGCGGTCAATTAACCTTGGTGGT 180
Db 145 CTCCTGGTGAATGAACACACCCGGTCAGTGAACCAACCATGGCGGTCAATTAACCTTGGTGGT 204
Qy 181 GTCACAGGTTTTCTGCTGACAGTGCATTCCTTGACCTACCTCAATCAAGAGACT 240
Db 205 GTCACAGGTTTTCTGCTGACAGTGCATTCCTTGACCTACCTCAATCAAGAGACT 264
Qy 241 TGGATGTTGGCTGCCCTCTTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTAC 300
Db 265 TGGATGTTGGCTGCCCTCTTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTAC 324
Qy 301 CTCACGTTCTTATCTATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 325 CTCACGTTCTTATCTATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
Qy 361 AAAGCAAAAGTGAATCTTACAGAAATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 385 AAAGCAAAAGTGAATCTTACAGAAATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 444
Qy 421 ACGTGGTGAATGTCATGTTGCTACCCCTGTTGCTCCCGTATGGAATCCATGAGAA 480
Db 445 ACGTGGTGAATGTCATGTTGCTACCCCTGTTGCTCCCGTATGGAATCCATGAGAA 504
Qy 481 TACATGAGGAGCACTGTTTAAATTTACAAAGAGTCTTACACATATGTAATC 540
Db 505 TACAAATGAGGAGCACTGTTTAAATTTACAAAGAGTCTTACACATATGTAATC 564
Qy 541 ATCAACTATATGATAGTCAATTTTGTGCTAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 565 ATCAACTATATGATAGTCAATTTTGTGCTAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
Qy 601 GTCCTCATCATATGTTGATGCTGAGAGCTACCCACTCTTACTATCCACAGAG 660
Db 625 GTCCTCATCATATGTTGATGCTGAGAGCTACCCACTCTTACTATCCACAGAG 684
Qy 661 TTCCTGGCTCAGCTGAAACACCTATTTTATAGGGTCACTCTTGTGTTGTTTCTCTTCCC 720
Db 685 TTCCTGGCTCAGCTGAAACACCTATTTTATAGGGTCACTCTTGTGTTGTTTCTCTTCCC 744
Qy 721 TACAGTCTCTTAGGATCTATTTACTGATGTTGAGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 745 TACAGTCTCTTAGGATCTATTTACTGATGTTGAGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 804
Qy 781 AAGGTTGATTTTATACCAATCTTCTGAGTAAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 805 AAGGTTGATTTTATACCAATCTTCTGAGTAAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 864
Qy 841 CTCCTCTTGTCTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Db 865 CTCCTCTTGTCTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 924
Qy 901 TGTGTTTGTGCGGT 915
Db 925 TGTGTTTGTGCGGT 939

RESULT 12
US-09-782-974C-21/c
; Sequence 21, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 41USPRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449

; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: Patent version 3.1
; SEQ ID NO 21
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-974C-21
Query Match 33.3%; Score 306; DB 10; Length 447;
Best Local Similarity 100.0%; Pred. No. 8.5e-151;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 60
Db 402 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 343
Qy 61 ATGAGCCTCTACTTCATAGTGTCTTATTTGGGGCTGTGGGTCTCATTTCCATCTTTTC 120
Db 342 ATGAGCCTCTACTTCATAGTGTCTTATTTGGGGCTGTGGGTCTCATTTCCATCTTTTC 283
Qy 121 CTCCTGGTGAATGAACACACCCGGTCAGTGAACCAACCATGGCGGTCAATTAACCTTGGTGGT 180
Db 282 CTCCTGGTGAATGAACACACCCGGTCAGTGAACCAACCATGGCGGTCAATTAACCTTGGTGGT 223
Qy 181 GTCACAGGTTTTCTGCTGACAGTGCATTCCTTGACCTTACCTCATCAAGAGACT 240
Db 222 GTCACAGGTTTTCTGCTGACAGTGCATTCCTTGACCTTACCTCATCAAGAGACT 163
Qy 241 TGGATGTTGGCTGCCCTCTTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTAC 300
Db 162 TGGATGTTGGCTGCCCTCTTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTAC 103
Qy 301 CTCACG 306
Db 102 CTCACG 97

RESULT 13
US-09-995-225-26/c
; Sequence 26, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
; FILE REFERENCE: ASEN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938

```

Db 12260 TACCAGTTCTTTAGGATCTATTACTGAATGTTGTGACGCAATCCCAATGCCGTGAACAGC 12319
QY 781 AAGTTGCAATTTTATAACGAATCTCTTGTAGTGTAAACAGCAATTAAGCTGCTATGATTTG 840
Db 12320 AAGTTGCAATTTTATAACGAATCTCTTGTAGTGTAAACAGCAATTAAGCTGCTATGATTTG 12379
QY 841 CTCTCTCTTTGCTTTTGGGGGAAGCCATTGTTTAAAGCAAAAGATAATTGGCTTTATGGAAT 900
Db 12380 CTCTCTCTTTGCTTTTGGGGGAAGCCATTGTTTAAAGCAAAAGATAATTGGCTTTATGGAAT 12439
QY 901 TGTGTTTTGTGCCGTTAG 918
Db 12440 TGTGTTTTGTGCCGTTAG 12457

RESULT 10
US-10-085-233B-1
; Sequence 1, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
; FILE REFERENCE: MPI2001-021P1RCP1M
; CURRENT APPLICATION NUMBER: US/10/085,233B
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (147)...(1085)
; OTHER INFORMATION: n at position 1384 can be any
; OTHER INFORMATION: nucleotide
US-10-085-233B-1

Query Match 94.4%; Score 867; DB 15; Length 1684;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCTGGCCACCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60
Db 171 ATGCCTGGCCACCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 230
QY 61 ATCAGCCTCTACTTCATAGTGTCTTATTTGGGGGCTGGTGGGTGTCTATTTCCATTTCTTTC 120
Db 231 ATCAGCCTCTACTTCATAGTGTCTTATTTGGGGGCTGGTGGGTGTCTATTTCCATTTCTTTC 290
QY 121 CTCTGTGTAAATGAACACCCGGTCAAGTACCAACCAATGGCGGTCAATTAACCTTGGTGGTG 180
Db 291 CTCTGTGTAAATGAACACCCGGTCAAGTACCAACCAATGGCGGTCAATTAACCTTGGTGGTG 350
QY 181 GTCCACAGCGTTTCTCTGTGACAGTCCATTTGGCTTTCACCTACCTCATCAAGAAAGACT 240
Db 351 GTCCACAGCGTTTCTCTGTGACAGTCCATTTGGCTTTCACCTACCTCATCAAGAAAGACT 410
QY 241 TGGATGTTGGGCTGCCCTCTCTGCAAAATTTGTAGTGCCCATGTGTGACATCCACATGTAC 300
Db 411 TGGATGTTGGGCTGCCCTCTCTGCAAAATTTGTAGTGCCCATGTGTGACATCCACATGTAC 470
QY 301 CTCACGTTCTCTATCTATGTTGGTATCTCTGTACACAGATACCTCATCTTCTTCAAGTGC 360
Db 471 CTCACGTTCTCTATCTATGTTGGTATCTCTGTACACAGATACCTCATCTTCTTCAAGTGC 530
QY 361 AAAGACAAAGTGAATTTCTACAGAAAATCTGCTGCTGTGGCTGCCAGTGTGTGCGATGTGG 420
Db 531 AAAGACAAAGTGAATTTCTACAGAAAATCTGCTGCTGTGGCTGCCAGTGTGTGCGATGTGG 590

```

```

QY 421 ACCTGGTGTATGTCTACCTCCCTGTTGTCTCCCGGTATGGAATCCCATGAGAA 480
Db 591 ACCTGGTGTATGTCTACCTCCCTGTTGTCTCCCGGTATGGAATCCCATGAGAA 650
QY 481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGAAAAATC 540
Db 651 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGAAAAATC 710
QY 541 ATCAACTATATGATGATGATTTTGTCTATAGCCGTTGCTGTGATTTCTGTTGGTCTTCCAG 600
Db 711 ATCAACTATATGATGATGATTTTGTCTATAGCCGTTGCTGTGATTTCTGTTGGTCTTCCAG 770
QY 601 GTCTTCATCATTTATGTTGATGTCAGAAAGCTAGCCACCTTTTACTATCCACAGAGAG 660
Db 771 GTCTTCATCATTTATGTTGATGTCAGAAAGCTAGCCACCTTTTACTATCCACAGAGAG 830
QY 661 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTCTCTTGTGTTCTTCTTCCC 720
Db 831 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTCTCTTGTGTTCTTCTTCCC 890
QY 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCCCTGTAAACAGC 780
Db 891 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCCCTGTAGCAGC 950
QY 781 AAGTTGCAATTTTATAACGAATCTCTTGTAGTGTAAACAGCAATTAAGCTGCTATGATTTG 840
Db 951 AAGTTGCAATTTTATAACGAATCTCTTGTAGTGTAAACAGCAATTAAGCTGCTATGATTTG 1010
QY 841 CTCTCTTTGTCTTTGGGGGAAGCAATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Db 1011 CTCTCTTTGTCTTTGGGGGAAGCAATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 1070
QY 901 TGTGTTTTGTGCCGTTAG 918
Db 1071 TGTGTTTTGTGCCGTTAG 1088

RESULT 11
US-10-085-233B-3
; Sequence 3, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
; FILE REFERENCE: MPI2001-021P1RCP1M
; CURRENT APPLICATION NUMBER: US/10/085,233B
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(939)
US-10-085-233B-3

Query Match 94.1%; Score 864; DB 15; Length 939;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCTGGCCACCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60
Db 25 ATGCCTGGCCACCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 84
QY 61 ATCAGCCTCTACTTCATAGTGTCTTATTTGGGGGCTGGTGGGTGTCTATTTCCATTTCTTTC 120
Db 85 ATCAGCCTCTACTTCATAGTGTCTTATTTGGGGGCTGGTGGGTGTCTATTTCCATTTCTTTC 144

```

```
Db 267 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCATGCTGCACATCCACATGTAC 326
Qy 301 CTCAGCTTCTTATCTATGTGTGATCCTCTGTCACAGATACCTCATCTTCTTCAAGTGC 360
Db 327 CTCAGTTCCTTATTTCTATGTGTGATCCTCTGTCACAGATACCTCATCTTCTTCAAGTGC 386
Qy 361 AAAGACAAAGTGGAAATTTACAGAAAACTGTCATGTGTGGTGCAGTGTGGCATGTGG 420
Db 387 AAAGACAAAGTGGAAATTTACAGAAAACTGTCATGTGTGGTGCAGTGTGGCATGTGG 446
Qy 421 AGCTGTGTGATGTCTATGTGTGTACCTCTGTTGTCTCCGGTATGGAATCCATCAGGAA 480
Db 447 AGCTGTGTGATGTCTATGTGTGTACCTCTGTTGTCTCCGGTATGGAATCCATCAGGAA 506
Qy 481 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTACACATATGTGAAAAATC 540
Db 507 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTACACATATGTGAAAAATC 566
Qy 541 ATCAACTATATGATGTCTATGTGTGTCTATGATGCTGTGATCTGTGCTTCCAG 600
Db 567 ATCAACTATATGATGTCTATGTGTGTCTATGATGCTGTGATCTGTGCTTCCAG 626
Qy 601 GTCTTCATCATTTATGTGTGTGAGAGCTTACGCCACTCTTTACTATCCACAGGAG 660
Db 627 GTCTTCATCATTTATGTGTGTGAGAGCTTACGCCACTCTTTACTATCCACAGGAG 686
Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTGATCTGTTGTTTCTTCC 720
Db 687 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTGATCTGTTGTTTCTTCC 746
Qy 721 TACCAGTTCCTTATGATCTTATTTACTTGAATGTGTGAGGCAATCCAAATGCCCTGTAACAGC 780
Db 747 TACCAGTTCCTTATGATCTTATTTACTTGAATGTGTGAGGCAATCCAAATGCCCTGTAACAGC 806
Qy 781 AAGGTGCAATTTTAAACGAATCTTCTTGTAGTGTAAAGCAATTTAGCTGTATGATTTG 840
Db 807 AAGGTGCAATTTTAAACGAATCTTCTTGTAGTGTAAAGCAATTTAGCTGTATGATTTG 866
Qy 841 CTCTCTTTTGTCTTTGGGGAGGCAATTTGTTTAAAGCAATTTAGCTGTATGATTTG 900
Db 867 CTCTCTTTTGTCTTTGGGGAGGCAATTTGTTTAAAGCAATTTAGCTGTATGATTTG 926
Qy 901 TGTGTTTGTGCGGTAG 918
Db 927 TGTGTTTGTGCGGTAG 944
```

RESULT 9

```
US-10-292-798-1007
; Sequence 1007, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABE, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: 2002-11-13
; PRIOR FILING DATE: 2001-12-18
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1007
; LENGTH: 113306
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
```

```
; FEATURE: (1)...(113306)
; LOCATION: (1)...(113306)
; NAME/KEY: CDS
; LOCATION: (201)...(207)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11526)...(12452)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37954)...(38097)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (98732)...(98784)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112891)...(113106)
; US-10-292-798-1007

Query Match 100.0%; Score 918; DB 16; Length 113306;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTGGCCACAAATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 60
Db 11540 ATGCTGTGGCCACAAATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 11599
Qy 61 ATCAGCCTCTTACTTCTATGTGTCTTATTTGGGGGCTGTGGGTGTCATTTCCATTTCTTTTC 120
Db 11600 ATCAGCCTCTTACTTCTATGTGTCTTATTTGGGGGCTGTGGGTGTCATTTCCATTTCTTTTC 11659
Qy 121 CTCCTGTGAAAAATGAACACCCCGGTGAGTGACACCACTGCGGTGCTTAACTTGGTGGTG 180
Db 11660 CTCCTGTGAAAAATGAACACCCCGGTGAGTGACACCACTGCGGTGCTTAACTTGGTGGTG 11719
Qy 181 GTCCAGACGCTTTTCTGTGTGACAGTGCCATTTGCGTTGACCTACCTCATCAAGAGACT 240
Db 11720 GTCCAGACGCTTTTCTGTGTGACAGTGCCATTTGCGTTGACCTACCTCATCAAGAGACT 11779
Qy 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCAATCCACATGTAC 300
Db 11780 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCAATCCACATGTAC 11839
Qy 301 CTCAGTTCCTTATCTATGTGTGTGATCTCTGGTCAACAGATACCTCATCTTCTTCAAGTGC 360
Db 11840 CTCAGTTCCTTATCTATGTGTGTGATCTCTGGTCAACAGATACCTCATCTTCTTCAAGTGC 11899
Qy 361 AAAGACAAAGTGGAAATTTCTACAGAAAACTGCATGTGTGGTGCAGTGTGCGATGTGG 420
Db 11900 AAAGACAAAGTGGAAATTTCTACAGAAAACTGCATGTGTGGTGCAGTGTGCGATGTGG 11959
Qy 421 AGCTGTGTGATGTCTATGTGTGTGATACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAA 480
Db 11960 AGCTGTGTGATGTCTATGTGTGTGATACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAA 12019
Qy 481 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAAAATC 540
Db 12020 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAAAATC 12079
Qy 541 ATCAACTATATGATGTCTATGTGTGTGATGCTGTGATCTGTGTTGGTCTTCCAG 600
Db 12080 ATCAACTATATGATGTCTATGTGTGTGATGCTGTGATCTGTGTTGGTCTTCCAG 12139
Qy 601 GTCTTCATCATTTATGTGTGTGAGAGCTTACGCCACTTCTTACTATCCACAGGAG 660
Db 12140 GTCTTCATCATTTATGTGTGTGAGAGCTTACGCCACTTCTTACTATCCACAGGAG 12199
Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTGATCTCTTGTGTTTCTTCC 720
Db 12200 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTGATCTCTTGTGTTTCTTCC 12259
Qy 721 TACCAGTTCCTTATGATCTTATTTACTTGAATGTGTGAGGCAATCCAAATGCCCTGTAACAGC 780
```



```

; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1193
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1318)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1118)
US-10-017-161-1193

Query Match      100.0%; Score 918; DB 15; Length 1318;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGCTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
DB 201 ATGCGCTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 260
QY 61 ATCAGCCTCTACTTCATAGTGTATTGCGGGCTGGTGGTGTCAATTCCTTTC 120
DB 261 ATCAGCCTCTACTTCATAGTGTATTGCGGGCTGGTGGTGTCAATTCCTTTC 320
QY 121 CTCCTGTGAATGAACACCCGGTCAGTGACACCATGGCGGTGCTATTAACCTTGGTGTG 180
DB 321 CTCCTGTGAATGAACACCCGGTCAGTGACACCATGGCGGTGCTATTAACCTTGGTGTG 380
QY 181 GTCCACAGCGTTTCTGTGTGACAGTGCATTTCCGTTGACCTACCTCATCAAGAGACT 240
DB 381 GTCCACAGCGTTTCTGTGTGACAGTGCATTTCCGTTGACCTACCTCATCAAGAGACT 440
QY 241 TGCATGTTGGGTGCGCTCTCCAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 300
DB 441 TGCATGTTGGGTGCGCTCTCCAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 500
QY 301 CTCACGTTCTATTTCTATGTGGTGATGCTGGTGCACAGATACCTCATCTTCTCAAGTGC 360
DB 501 CTCACGTTCTATTTCTATGTGGTGATGCTGGTGCACAGATACCTCATCTTCTCAAGTGC 560
QY 361 AAGACAAAGTGAATTTACACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 561 AAGACAAAGTGAATTTACACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
QY 421 ACCTGTGTGATTTGCTATTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 621 ACCTGTGTGATTTGCTATTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
QY 481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAATTC 540
DB 681 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAATTC 740
QY 541 ATCAACTATATAGTATGCTATTTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 741 ATCAACTATATAGTATGCTATTTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
QY 601 GTCTTCATCATATATGTTGCTGCAAGCTACGCACTCTTCTTACTATCCACACAGGAG 660
DB 801 GTCTTCATCATATATGTTGCTGCAAGCTACGCACTCTTCTTACTATCCACACAGGAG 860
QY 661 TTCTGGCTCAGCTGAAACCTATTTTATAGGGGTCACTCTGTTTGTCTTCTTCTTCTTCTTCT 720
DB 861 TTCTGGCTCAGCTGAAACCTATTTTATAGGGGTCACTCTGTTTGTCTTCTTCTTCTTCTTCT 920
QY 721 TACCAGTCTTTAGGATCTATTTACTTGAATTTGTGTGACGCAATTCCTCAATGCTGTAAACAG 780
DB 921 TACCAGTCTTTAGGATCTATTTACTTGAATTTGTGTGACGCAATTCCTCAATGCTGTAAACAG 980
QY 781 AAGTTGCAATTTATACGAATCTTCTGAGTGAACAGCAATTTAGCTGCTATGATTG 840
DB 981 AAGTTGCAATTTATACGAATCTTCTGAGTGAACAGCAATTTAGCTGCTATGATTG 1040

```

```

QY 841 CTTCTCTTTGTCTTTGGGAGCCCAATTCGTTTAAAGAAAAGATATTCGCTTATGGAAT 900
DB 1041 CTTCTCTTTGTCTTTGGGAGCCCAATTCGTTTAAAGAAAAGATATTCGCTTATGGAAT 1100
QY 901 TGTGTTTGTGCGGTAG 918
DB 1101 TGTGTTTGTGCGGTAG 1118

RESULT 8
US-09-782-974C-81
; Sequence 81, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 2525
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-974C-81

```

```

Query Match      100.0%; Score 918; DB 10; Length 2525;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
DB 27 ATGCGTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 86
QY 61 ATCAGCCTCTACTTCATAGTGTATTGCGGGCTGGTGGTGTCAATTCCTTTC 120
DB 87 ATCAGCCTCTACTTCATAGTGTATTGCGGGCTGGTGGTGTCAATTCCTTTC 146
QY 121 CTCCTGTGAAATGAACACCCGGTCAGTGACACCATGGCGGTCAATTAACCTTGGTGTG 180
DB 147 CTCCTGTGAAATGAACACCCGGTCAGTGACACCATGGCGGTCAATTAACCTTGGTGTG 206
QY 181 GTCCACAGCGTTTCTGCTGACAGTGCATTTGCTTGACTACCTCATCAAGAGACT 240
DB 207 GTCCACAGCGTTTCTGCTGACAGTGCATTTGCTTGACTACCTCATCAAGAGACT 266
QY 241 TGCATGTTGGGTGCGCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCCATGTAC 300

```

361	AAAGCAAGTGGAAATTCACAGAAACTGCATGCTGTGCTGCCAGTCTGGCATGTGG	420
421	ACGCTGGTGATTTGTCATTGTGTTACCCCTGGTTGTCTCCCGGTATGGAATCCATGAGGAA	480
421	ACGCTGGTGATTTGTCATTGTGTTACCCCTGGTTGTCTCCCGGTATGGAATCCATGAGGAA	480
481	TACAATGAGGAGCACTGTTTAAATTTTACAAAGAGCTTGCTTACACATATGTGAAATC	540
481	TACAATGAGGAGCACTGTTTAAATTTTACAAAGAGCTTGCTTACACATATGTGAAATC	540
541	ATCAACTATATGATAGTCATTTTGTTCATAGCCCTTGCTGTGATCTGTGTGCTTTCCAG	600
541	ATCAACTATATGATAGTCATTTTGTTCATAGCCCTTGCTGTGATCTGTGTGCTTTCCAG	600
601	GTCTTCATCATATTTGTGATGGTGAGAGCTAGCCCACTCTTTACTATCCCAACCAAGG	660
601	GTCTTCATCATATTTGTGATGGTGAGAGCTAGCCCACTCTTTACTATCCCAACCAAGG	660
661	TTCTCGGCTCAGCTCAAAAACCTATTTTATAGGGGTCACTCTGTGTGTTTCCCTTCCC	720
661	TTCTCGGCTCAGCTCAAAAACCTATTTTATAGGGGTCACTCTGTGTGTTTCCCTTCCC	720
721	TACCAGTCTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAAATGCCTGTAAACAG	780
721	TACCAGTCTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAAATGCCTGTAAACAG	780
781	AAGGTTGCATTTTATTAAGCAAAATCTTCTTCGAGTGTACACAAATTAAGCTCATGATTTG	840
781	AAGGTTGCATTTTATTAAGCAAAATCTTCTTCGAGTGTACACAAATTAAGCTCATGATTTG	840
841	CTTCTCTTTTGTCTTTGGGGGAGGCCATTTGGTTTAAAGCAAAAGATAAATGGCTTATGGAAT	900
841	CTTCTCTTTTGTCTTTGGGGGAGGCCATTTGGTTTAAAGCAAAAGATAAATGGCTTATGGAAT	900
901	TGTGTTTGTGCCGTTAG	918
901	TGTGTTTGTGCCGTTAG	918

RESULT 6

RESULT 6
 US-10-293-171-1
 / Sequence 1, Application US/10293171
 / Publication No. US20030138418A1
 / GENERAL INFORMATION:
 / APPLICANT: Eishingdrelo, Haifeng
 / APPLICANT: Cai, Jidong
 / APPLICANT: Gassenhuber, Johann
 / TITLE OF INVENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND USES TH
 / FILE REFERENCE: USAV2001/0158 US NP
 / CURRENT APPLICATION NUMBER: US/10/293,171
 / CURRENT FILING DATE: 2002-11-13
 / PRIOR APPLICATION NUMBER: US60/354,150
 / PRIOR FILING DATE: 2001-11-13
 / NUMBER OF SEQ ID NOS: 9
 / SOFTWARE: Patentin version 3.1
 / SEQ ID NO 1
 / LENGTH: 1040
 / TYPE: DNA
 / ORGANISM: homo sapiens
 US-10-293-171-1

	Query Match	100.0%	Score 918;	DB 15;	Length 1040;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 918;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	ATGCGCTGGCCAAATACCTCCAGGAATTCCTCTTGGCATCCTATAGTGACACCCCACTTA	60		
Db	1	ATGCGCTGGCCAAATACCTCCAGGAATTCCTCTTGGCATCCTATAGTGACACCCCACTTA	60		
Qy	61	ATCAGGCTCTACTTCATATAGTGTTATTGGCGGGCTGGTGGGTGTCATTTCCATTCCTTTTC	120		
Db	61	ATCAGGCTCTACTTCATATAGTGTTATTGGCGGGCTGGTGGGTGTCATTTCCATTCCTTTTC	120		

RESULT 7
US-10-017-161-1193
; Sequence 1193, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18

```
; Sequence 1, Application US/10055106C
; Publication No. US20030017536A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: FC10970AGLK
; CURRENT APPLICATION NUMBER: US/10/055,106C
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: GB0101739.1
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/267,341
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-055-106C-1

Query Match 100.0%; Score 918; DB 13; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCTGGCCACATACCTCCAGGAATTCCTTGGATCCTATAGTACACCCCACTTA 60
DB 1 ATGCCTGGCCACATACCTCCAGGAATTCCTTGGATCCTATAGTACACCCCACTTA 60

QY 61 ATCAGCCTCTACTTTCATAGTGCCTTATGGGGGGTGGTGGTGTCTATTTCTTTTC 120
DB 61 ATCAGCCTCTACTTTCATAGTGCCTTATGGGGGGTGGTGGTGTCTATTTCTTTTC 120

QY 121 CTCCTGTGAAATGAAACACCCGGTCACTGACACCACTGCGGTCACTTAATTTGGTGG 180
DB 121 CTCCTGTGAAATGAAACACCCGGTCACTGACACCACTGCGGTCACTTAATTTGGTGG 180

QY 181 GTCCACAGAGCTGTTTCTGCTGACAGTGCCTTGGCTTGGCTTGGCTTGGCTTGGCTT 240
DB 181 GTCCACAGAGCTGTTTCTGCTGACAGTGCCTTGGCTTGGCTTGGCTTGGCTTGGCTT 240

QY 241 TGGATGTTTGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGACATCCCATGATAC 300
DB 241 TGGATGTTTGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGACATCCCATGATAC 300

QY 301 CTCAGGCTTCCTATTCTATGTGGTGTATCTGTGTCACAGATACCTCATCTTCTCAAGTGC 360
DB 301 CTCAGGCTTCCTATTCTATGTGGTGTATCTGTGTCACAGATACCTCATCTTCTCAAGTGC 360

QY 361 AAAGACAAAGTGGAAATCTACAGAAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 AAAGACAAAGTGGAAATCTACAGAAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 421 ACGCTGTGATGTCATGTTGGTACCCCTGGTGTCTCCCGGTATGAAATCCATGAGGAA 480
DB 421 ACGCTGTGATGTCATGTTGGTACCCCTGGTGTCTCCCGGTATGAAATCCATGAGGAA 480

QY 481 TACAATGAGGAGCACTGTTTAAATTTACAAAGAGCTTCTTACACATATGTGAAATC 540
DB 481 TACAATGAGGAGCACTGTTTAAATTTACAAAGAGCTTCTTACACATATGTGAAATC 540

QY 541 ATCAACTATATGATGATTTTGTATAGCCGTTGCTGTGATTCGTTGGTCTTCCAG 600
DB 541 ATCAACTATATGATGATTTTGTATAGCCGTTGCTGTGATTCGTTGGTCTTCCAG 600

QY 601 GTCTTCATCATATTATGTTGATGGTGCAGAGCTAGCCACTCTTTACTATCCACAGGAG 660
DB 601 GTCTTCATCATATTATGTTGATGGTGCAGAGCTAGCCACTCTTTACTATCCACAGGAG 660

QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTATCTTGTGTTCTTCTTCC 720
DB 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTATCTTGTGTTCTTCTTCC 720
```

RESULT 5

```
US-10-188-405-9
; Sequence 9, Application US/10188405
; Publication No. US20030082585A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Dai, Kang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Zhao, Jiagang
; APPLICANT: Zhai, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030082585A1:el Receptors
; FILE REFERENCE: 018781-00841005
; CURRENT APPLICATION NUMBER: US/10/188,405
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR343
US-10-188-405-9
```

```
Query Match 100.0%; Score 918; DB 15; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCTGGCCACATACCTCCAGGAATTCCTTGGATCCTATAGTACACCCCACTTA 60
DB 1 ATGCCTGGCCACATACCTCCAGGAATTCCTTGGATCCTATAGTACACCCCACTTA 60

QY 61 ATCAGCCTCTACTTTCATAGTGCCTTATGGGGGGTGGTGGTGTCTATTTCTTTTC 120
DB 61 ATCAGCCTCTACTTTCATAGTGCCTTATGGGGGGTGGTGGTGTCTATTTCTTTTC 120

QY 121 CTCCTGTGAAATGAAACACCCGGTCACTGACACCACTGCGGTCACTTAATTTGGTGG 180
DB 121 CTCCTGTGAAATGAAACACCCGGTCACTGACACCACTGCGGTCACTTAATTTGGTGG 180

QY 181 GTCCACAGAGCTGTTTCTGCTGACAGTGCCTTGGCTTGGCTTGGCTTGGCTTGGCTT 240
DB 181 GTCCACAGAGCTGTTTCTGCTGACAGTGCCTTGGCTTGGCTTGGCTTGGCTTGGCTT 240

QY 241 TGGATGTTTGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGACATCCCATGATAC 300
DB 241 TGGATGTTTGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGACATCCCATGATAC 300

QY 301 CTCAGGCTTCCTATTCTATGTGGTGTATCTGTGTCACAGATACCTCATCTTCTCAAGTGC 360
DB 301 CTCAGGCTTCCTATTCTATGTGGTGTATCTGTGTCACAGATACCTCATCTTCTCAAGTGC 360

QY 361 AAAGACAAAGTGGAAATCTTACAGAAAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
```

241 TGGATGTTTGGCTGCGCTCTGCAAAATTTGTGAGTGGCCATGCTGCACATCCACATGTAC 300
Db |||||
241 TGGATGTTTGGCTGCGCTCTGCAAAATTTGTGAGTGGCCATGCTGCACATCCACATGTAC 300
Qy CTCAGCTTCCTATTTCTATGTGTGTGATCTCTGTCACAGATACCTCATCTCTTCAAGTGC 360
Db |||||
301 CTCAGCTTCCTATTTCTATGTGTGTGATCTCTGTCACAGATACCTCATCTCTTCAAGTGC 360
Qy |||||
361 AAAGCAAAAGTGGATTTCTACAGAAATCTGATGCTGTGGCTGCCAGTGGCATGTGG 420
Db |||||
361 AAAGCAAAAGTGGATTTCTACAGAAATCTGATGCTGTGGCTGCCAGTGGCATGTGG 420
Qy AGCTGGTGAATGTCATGTGTGTGATCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480
Db |||||
421 AGCTGGTGAATGTCATGTGTGTGATCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480
Qy |||||
481 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAAATC 540
Db |||||
481 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAAATC 540
Qy ATCAACTATATGATAGTCAATTTTGTGATGCGCTTGTGATGCTGTGATCTGTCTTCCAG 600
Db |||||
541 ATCAACTATATGATAGTCAATTTTGTGATGCGCTTGTGATGCTGTGATCTGTCTTCCAG 600
Qy |||||
601 GTCTTCATCATTTATGTTGATGCTGAGAGCTACGCCACTCTTACTATCCACCAGGAG 660
Db |||||
601 GTCTTCATCATTTATGTTGATGCTGAGAGCTACGCCACTCTTACTATCCACCAGGAG 660
Qy |||||
661 TTCTGGGCTCAGCTGAAACACCTATTTTATAGGGGTCACTCTTGTGTTTGTCTTCC 720
Db |||||
661 TTCTGGGCTCAGCTGAAACACCTATTTTATAGGGGTCACTCTTGTGTTTGTCTTCC 720
Qy |||||
721 TACCAAGTCTTTAGGATCTATTTACTTGAATGTTGAGCAGTTCAGATCCAGTCCCTGTAACAGC 780
Db |||||
721 TACCAAGTCTTTAGGATCTATTTACTTGAATGTTGAGCAGTTCAGATCCAGTCCCTGTAACAGC 780
Qy |||||
781 AAGGTTGCAATTTTAAACGAAATCTTCTGAGTGTAAAGCAATGAGTCTATGATTTG 840
Db |||||
781 AAGGTTGCAATTTTAAACGAAATCTTCTGAGTGTAAAGCAATGAGTCTATGATTTG 840
Qy |||||
841 CTCTCTTTGCTTTTGGGGAGGCAATGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT 900
Db |||||
841 CTCTCTTTGCTTTTGGGGAGGCAATGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT 900
Qy |||||
901 TGTGTTTGTGCGGTTAG 918
Db |||||
901 TGTGTTTGTGCGGTTAG 918

RESULT 3

US-10-297-908A-2
; Sequence 2, Application US/10297908A
; Publication No. US20040029793A1
; GENERAL INFORMATION:
; APPLICANT: MORIYA, Takeo
; APPLICANT: ITO, Takahashi
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: MIYAJIMA, No. US20040029793A1uyuki
; TITLE OF INVENTION: No. US20040029793A1el G Protein-Coupled Receptor Protein and its
; FILE REFERENCE: 2737 USOP
; CURRENT APPLICATION NUMBER: US/10/297, 908A
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: PCT/JP01/05061
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: JP 2000-184596
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: JP 2000-223887
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Human

US-10-297-908A-2
Query Match 100.0%; Score 918; DB 13; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
Db 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
Qy 61 ATCAGCCTCTACCTTCAATAGTCTTATTTGGCGGCTGTGGTGTCTCATTTTCCATTTCTTTC 120
Db 61 ATCAGCCTCTACCTTCAATAGTCTTATTTGGCGGCTGTGGTGTCTCATTTTCCATTTCTTTC 120
Qy 121 CTCCTGTGAAAAATGAACACCCGGTCACTGACACCAATGGCGGTCAATTAACCTTGGTGTG 180
Db 121 CTCCTGTGAAAAATGAACACCCGGTCACTGACACCAATGGCGGTCAATTAACCTTGGTGTG 180
Qy 181 GTCCACAGCCTTTTCTGCTGACAGTGCCTTTGCTTGCCTACCTCATCTCAACAGAGACT 240
Db 181 GTCCACAGCCTTTTCTGCTGACAGTGCCTTTGCTTGCCTACCTCATCTCAACAGAGACT 240
Qy 241 TGGATGTTTGGGCTGCGCTTCTGCAAAATTTGTGAGTGCCTATGCTGCACATCCACATGTAC 300
Db 241 TGGATGTTTGGGCTGCGCTTCTGCAAAATTTGTGAGTGCCTATGCTGCACATCCACATGTAC 300
Qy 301 CTCACGTTCTTATTTATGTTGTTGATCTCTGTCACAGATACCTCATCTCTTCTTCAAGTGC 360
Db 301 CTCACGTTCTTATTTATGTTGTTGATCTCTGTCACAGATACCTCATCTCTTCTTCAAGTGC 360
Qy 361 AAAGCAAAAGTGGATTTCTACAGAAATCTGATGCTGTGGCTGCCAGTGGCATGTGG 420
Db 361 AAAGCAAAAGTGGATTTCTACAGAAATCTGATGCTGTGGCTGCCAGTGGCATGTGG 420
Qy 421 ACGCTGTGATTTGTCATGTTGTTGATACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480
Db 421 ACGCTGTGATTTGTCATGTTGTTGATACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480
Qy 481 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTCTTACACATATGTGAAATC 540
Db 481 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTCTTACACATATGTGAAATC 540
Qy 541 ATCAACTATATGATAGTCAATTTTGTGATGCGCTTGTGATCTGTGTTGGTCTTCCAG 600
Db 541 ATCAACTATATGATAGTCAATTTTGTGATGCGCTTGTGATCTGTGTTGGTCTTCCAG 600
Qy 601 GTCTTCATCATTTATGTTGATGCTGAGAGCTACGCCACTCTTACTATCCACCAGGAG 660
Db 601 GTCTTCATCATTTATGTTGATGCTGAGAGCTACGCCACTCTTACTATCCACCAGGAG 660
Qy 661 TTCTGGGCTCAGCTGAAACACCTATTTTATAGGGGTCACTCTTGTGTTTGTCTTCC 720
Db 661 TTCTGGGCTCAGCTGAAACACCTATTTTATAGGGGTCACTCTTGTGTTTGTCTTCC 720
Qy 721 TACCAAGTCTTTAGGATCTATTTACTTGAATGTTGAGCAGTTCAGATCCAGTCCCTGTAACAGC 780
Db 721 TACCAAGTCTTTAGGATCTATTTACTTGAATGTTGAGCAGTTCAGATCCAGTCCCTGTAACAGC 780
Qy 781 AAGGTTGCAATTTTAAACGAAATCTTCTGAGTGTAAAGCAATGAGTCTATGATTTG 840
Db 781 AAGGTTGCAATTTTAAACGAAATCTTCTGAGTGTAAAGCAATGAGTCTATGATTTG 840
Qy 841 CTCTCTTTGCTTTTGGGGAGGCAATGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT 900
Db 841 CTCTCTTTGCTTTTGGGGAGGCAATGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT 900
Qy 901 TGTGTTTGTGCGGTTAG 918
Db 901 TGTGTTTGTGCGGTTAG 918

RESULT 4

US-10-055-106C-1

;; PRIOR APPLICATION NUMBER: 60/309,208
;; PRIOR FILING DATE: 2001-07-31
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 918
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-995-225-3

Query Match 100.0%; Score 918; DB 9; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCTGGCCACATACCTCCAGGAATTCCTTGGAGATCCTATAGTGACACCCCACTTA	60
Db	1	ATGCTGGCCACATACCTCCAGGAATTCCTTGGAGATCCTATAGTGACACCCCACTTA	60
Qy	61	ATCAGCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGTGCATTTCCATTCCTTTTC	120
Db	61	ATCAGCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGTGCATTTCCATTCCTTTTC	120
Qy	121	CTCTCGTGAATAATGAACACCCGCTCAGTGACACCAATGGCGGTCAATTAATCTTGGTGG	180
Db	121	CTCTCGTGAATAATGAACACCCGCTCAGTGACACCAATGGCGGTCAATTAATCTTGGTGG	180
Qy	181	GTCCACAGGCTTTTCTGCTGACGTGCATTTCCGCTTACCTCATCAAGAGACT	240
Db	181	GTCCACAGGCTTTTCTGCTGACGTGCATTTCCGCTTACCTCATCAAGAGACT	240
Qy	241	TGGATGTTGGGCTGGCCCTCTGCAAAATTTGTAGTGCCATGTCACATCCACATGTAC	300
Db	241	TGGATGTTGGGCTGGCCCTCTGCAAAATTTGTAGTGCCATGTCACATCCACATGTAC	300
Qy	301	CTCAGTTCCTATCTATGTTGGTGCATCTGGTCAACAGATCCTCATCTTCAAGTGC	360
Db	301	CTCAGTTCCTATCTATGTTGGTGCATCTGGTCAACAGATCCTCATCTTCAAGTGC	360
Qy	361	AAACACAAGTGAATTTCTACAGAAATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG	420
Db	361	AAACACAAGTGAATTTCTACAGAAATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG	420
Qy	421	ACGCTGGTGAATTCATGTTGGTACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
Db	421	ACGCTGGTGAATTCATGTTGGTACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
Qy	481	TACATGAGGAGCTGTTTAAATTTTCAAAAGAGCTTGTACATATGTGAAATC	540
Db	481	TACATGAGGAGCTGTTTAAATTTTCAAAAGAGCTTGTACATATGTGAAATC	540
Qy	541	ATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	600
Db	541	ATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	600
Qy	601	GTCTTCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	660
Db	601	GTCTTCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	660
Qy	661	TTCTGGGCTCAGCTGAAACCTATTTTATAGGGTTCATCTTGTGTTGTTCTTCTTCCC	720
Db	661	TTCTGGGCTCAGCTGAAACCTATTTTATAGGGTTCATCTTGTGTTGTTCTTCTTCCC	720
Qy	721	TACAGTTCCTTTAGATCTATATCTTGAATGTTGTGACGATTCCTATGCTGTAAAGC	780
Db	721	TACAGTTCCTTTAGATCTATATCTTGAATGTTGTGACGATTCCTATGCTGTAAAGC	780
Qy	781	AAGTTGATTTTATACGAAATCTTCTTGAATGTTGTGACGATTCCTATGCTGTAAAGC	840
Db	781	AAGTTGATTTTATACGAAATCTTCTTGAATGTTGTGACGATTCCTATGCTGTAAAGC	840
Qy	841	CTTCTTTTGTCTTTGGGGAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT	900
Db	841	CTTCTTTTGTCTTTGGGGAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT	900

RESULT 2

US-09-995-225-3
; Sequence 3, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human C
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-225-3

Query Match 100.0%; Score 918; DB 10; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCTGGCCACATACCTCCAGGAATTCCTTGGAGATCCTATAGTGACACCCCACTTA	60
Db	1	ATGCTGGCCACATACCTCCAGGAATTCCTTGGAGATCCTATAGTGACACCCCACTTA	60
Qy	61	ATCAGCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGTGCATTTCCATTCCTTTTC	120
Db	61	ATCAGCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGTGCATTTCCATTCCTTTTC	120
Qy	121	CTCTCGTGAATAATGAACACCCGCTCAGTGACACCAATGGCGGTCAATTAATCTTGGTGG	180
Db	121	CTCTCGTGAATAATGAACACCCGCTCAGTGACACCAATGGCGGTCAATTAATCTTGGTGG	180
Qy	181	GTCCACAGGCTTTTCTGCTGACGTGCATTTCCGCTTACCTCATCAAGAGACT	240
Db	181	GTCCACAGGCTTTTCTGCTGACGTGCATTTCCGCTTACCTCATCAAGAGACT	240

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 17:54:09 ; Search time 460 Seconds

(without alignments)
8997.651 Million cell updates/sec

Title: US-10-055-106c-1

Perfect score: 918

Sequence: 1 atgctggccacaatacctc.....attgtgtttgtgcgtag 918

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2907579 seqs, 2254313464 residues

Word size : 12

Total number of hits satisfying chosen parameters: 299695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

```
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	918	100.0	918	9	US-09-995-225-3
2	918	100.0	918	10	US-09-995-225-3
3	918	100.0	918	13	US-10-297-908A-2
4	918	100.0	918	13	US-10-055-106C-1
5	918	100.0	918	15	US-10-188-405-9
6	918	100.0	1040	15	US-10-293-171-1
7	918	100.0	1318	15	US-10-017-161-1193
8	918	100.0	2525	15	US-09-782-974C-81
9	918	100.0	113306	16	US-10-292-798-1007
10	867	94.4	1684	15	US-10-085-233B-1
11	864	94.1	939	15	US-10-085-233B-3
12	306	33.3	447	10	US-09-782-974C-21
13	29	3.2	29	9	US-09-995-225-26
14	29	3.2	29	10	US-09-995-225-26

c 15	28	3.1	28	9	US-09-995-225-25	Sequence 25, Appl
c 16	28	3.1	28	10	US-09-995-225-25	Sequence 25, Appl
c 17	27	2.9	810	15	US-10-366-504-1	Sequence 1, Appl
c 18	26	2.8	26	9	US-09-995-225-54	Sequence 54, Appl
c 19	26	2.8	26	10	US-09-995-225-54	Sequence 54, Appl
c 20	26	2.8	26	13	US-10-297-908A-7	Sequence 7, Appl
c 21	25	2.7	25	15	US-10-293-171-7	Sequence 7, Appl
c 22	24	2.6	24	10	US-09-782-974C-135	Sequence 135, Appl
c 23	24	2.6	24	10	US-09-782-974C-164	Sequence 164, Appl
c 24	24	2.6	24	13	US-10-297-908A-4	Sequence 4, Appl
c 25	24	2.6	24	15	US-10-293-171-5	Sequence 5, Appl
c 26	24	2.6	24	9	US-09-995-225-23	Sequence 23, Appl
c 27	24	2.6	24	10	US-09-995-225-23	Sequence 23, Appl
c 28	24	2.6	24	10	US-09-782-974C-136	Sequence 136, Appl
c 29	24	2.6	24	10	US-09-782-974C-165	Sequence 165, Appl
c 30	23	2.5	23	10	US-09-782-974C-137	Sequence 137, Appl
c 31	23	2.5	23	10	US-09-782-974C-166	Sequence 166, Appl
c 32	23	2.5	23	15	US-10-188-405-23	Sequence 23, Appl
c 33	23	2.5	31	9	US-09-995-225-24	Sequence 24, Appl
c 34	23	2.5	31	9	US-09-995-225-55	Sequence 55, Appl
c 35	23	2.5	31	10	US-09-995-225-24	Sequence 55, Appl
c 36	23	2.5	31	10	US-09-995-225-55	Sequence 55, Appl
c 37	23	2.5	34	10	US-09-782-974C-112	Sequence 112, Appl
c 38	22	2.4	22	13	US-10-297-908A-3	Sequence 3, Appl
c 39	22	2.4	22	15	US-10-188-405-22	Sequence 22, Appl
c 40	22	2.4	22	15	US-10-293-171-6	Sequence 6, Appl
c 41	21	2.3	21	13	US-10-297-908A-5	Sequence 5, Appl
c 42	21	2.3	21	15	US-10-293-171-3	Sequence 3, Appl
c 43	21	2.3	21	15	US-10-293-171-4	Sequence 4, Appl
c 44	21	2.3	21	15	US-10-293-171-8	Sequence 8, Appl
c 45	21	2.3	21	15	US-10-293-171-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

```
US-09-995-225-3
; Sequence 3, Application US/0995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
```

ACCESSION AX451925
VERSION AX451925.1 GI:21698748
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baughn, M.R., Graul, R.C., Walia, N.K., Gandhi, A.R., Hafalia, A.J.,
Ranumkar, J., Tribouley, C.M., Thornton, M., Rallick, D.A., Yao, M.G.,
Elliot, V.S., Burford, N., Khan, F.A., Yue, H., Lu, Y., Arvizu, C.,
Roope, R., Nguyen, D.B., Lee, E.A., Lu, D.A., Ison, C.H., Walsh, R.T. and
Policky, J.L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0226825-A 22 04-APR-2002;
Incyte Genomics, Inc. (US)
FEATURES
source
1..1499
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 6157025CB1"

ORIGIN
Query Match 97.5%; Score 895; DB 6; Length 1499;
Best Local Similarity 99.9%; Pred. No. 1.5e-219;
Matches 906; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ATGCGTGGCCCAATACCTCCAGGAATCTCTTGGATCGATATAGTGACACCCCACTTA 60
DB 381 ATGCGTGGCCCAATACCTCCAGGAATCTCTTGGATCGATATAGTGACACCCCACTTA 440
QY 61 ATCAGCCTCTACTTCATAGTGTCTTATGCGGGCTGGTGGGTGTCATTCCTCTTTTC 120
DB 441 ATCAGCCTCTACTTCATAGTGTCTTATGCGGGCTGGTGGGTGTCATTCCTCTTTTC 500
QY 121 CTCCTGGTGAATAACACCGGTCAGTGACCCAGTCCAGTGGCGGTCAATTAAGTGGTGG 180
DB 501 CTCCTGGTGAATAACACCGGTCAGTGACCCAGTGGCGGTCAATTAAGTGGTGGT 560
QY 181 GTCCACAGCGTTTCTCTGTCAGTGCCTTGGCTTGAACCTACCTCATCAAGAAGACT 240
DB 561 GTCCACAGCGTTTCTCTGTCAGTGCCTTGGCTTGAACCTACCTCATCAAGAAGACT 620
QY 241 TGGATGTTTGGCTGCCCTTCTGCAATTTGTAGTGCCATGCTGCACATCCACATGTAC 300
DB 621 TGGATGTTTGGCTGCCCTTCTGCAATTTGTAGTGCCATGCTGCACATCCACATGTAC 680
QY 301 CTCAGGTTCCCTATTCTATGTGGTGATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 360
DB 681 CTCAGGTTCCCTATTCTATGTGGTGATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 740
QY 361 AAAGACAAAGTGGAAATCTACAGAAAATGTCATGCTGGCTGGCAGTGGCGATGTGG 420
DB 741 AAAGACAAAGTGGAAATCTACAGAAAATGTCATGCTGGCTGGCAGTGGCGATGTGG 800
QY 421 AGCGTGGTGATTTGTCATTTGTTGCTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480
DB 801 AGCGTGGTGATTTGTCATTTGTTGCTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 860
QY 481 TACAAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 540
DB 861 TACAAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 920
QY 541 ATCAACTATATAGTATGATTTTGTCTATAGCGTGTCTGTGATCTGTGGTCTTCCAG 600
DB 921 ATCAACTATATAGTATGATTTTGTCTATAGCGTGTCTGTGATCTGTGGTCTTCCAG 980
QY 601 GTCTTCATCATTTATGTTGATGGTGAAGGTACGCCACTCTTTACTATCCCAAGGAG 660
DB 981 GTCTTCATCATTTATGTTGATGGTGAAGGTACGCCACTCTTTACTATCCCAAGGAG 1040
QY 661 TTCTGGGCTCAGTGAAAAACCTATTTTATAGGGGTATCCTTGTGTTTCTCTCC 720

DB 1041 TTCTGGGCTCAGCTGAARACCTATTTTATAGGGGTGATCTCTGTTGTTTCTCTCC 1100
QY 721 TACAGTTCCTTTAGGATCTATTAATCTTGAATGTTGTGACGCAATCCCAATGCTGTAAACAGC 780
DB 1101 TACAGTTCCTTTAGGATCTATTAATCTTGAATGTTGTGACGCAATCCCAATGCTGTAAACAGC 1160
QY 781 AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAAACAGCAATTAAGCTGCTATGATTG 840
DB 1161 AAGTGGCATTTTATAACGAAATCTTCTTGAGTGTAAACAGCAATTAAGCTGCTATGATTG 1220
QY 841 CTCTCTCTTGTCTTTTGGGGAAGCCATTTGTTAAAGCAAAAGATAAATGGCTTATGGAAT 900
DB 1221 CTCTCTCTTGTCTTTTGGGGAAGCCATTTGTTAAAGCAAAAGATAA-TGGCTTATGGAAT 1279
QY 901 TGTGTTT 907
DB 1280 TGTGTTT 1286

Search completed: April 25, 2004, 16:55:13
Job time : 3934 secs

QY 361 AAGACAAAGTGGAAATCTACAGAAATCTGCTGTGGCTGCCAGTCTGGCATGGG 420
Db 133483 AAGACAAAGTGGAAATCTACAGAAATCTGCTGTGGCTGCCAGTGGG 133542
QY 421 AGCTGGTGAATGTCATTTGCTGACCCCTGGTGTCTCCGGTATGGAAATCCATGAGAA 480
Db 133543 AGCTGGTGAATGTCATTTGCTGACCCCTGGTGTCTCCGGTATGGAAATCCATGAGAA 133602
QY 481 TACAATGAGGAGCAGCTGTTTAAATTTACAAAGAGCTTGTCTACACATATGTGAAATC 540
Db 133603 TACAATGAGGAGCAGCTGTTTAAATTTACAAAGAGCTTGTCTACACATATGTGAAATC 133662
QY 541 ATCAACTATATGATGATGATTTTGTGATGAGCGCTTGTGATGCTGTGCTTCCAG 600
Db 133663 ATCAACTATATGATGATGATTTTGTGATGAGCGCTTGTGATGCTGTGCTTCCAG 133722
QY 601 GTCCTCATCATTTATGTTGATGTTGAGAGCTACGCCACTCTTTACTATCCACACAGAG 660
Db 133723 GTCCTCATCATTTATGTTGATGTTGAGAGCTACGCCACTCTTTACTATCCACACAGAG 133782
QY 661 TTCGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTTTGTTTCTTCC 720
Db 133783 TTCGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTTTGTTTCTTCC 133842
QY 721 TACCAGTCTTTAGGATCTATTTACTTGAATGTTGAGCGCATCCCAATGCTGTGAAAT 780
Db 133843 TACCAGTCTTTAGGATCTATTTACTTGAATGTTGAGCGCATCCCAATGCTGTGAAAT 133902
QY 781 AAGGTTGCAATTTTAAACCAATCTTTGAGTGTAAACAGCAATTAGCTGTATGATTG 840
Db 133903 AAGGTTGCAATTTTAAACCAATCTTTGAGTGTAAACAGCAATTAGCTGTATGATTG 133962
QY 841 CTTCTCTTTGCTTTGGGGAGGCAATGTTGTTAAGCAAAAGATTAATGGCTTATGGAAT 900
Db 133963 CTTCTCTTTGCTTTGGGGAGGCAATGTTGTTAAGCAAAAGATTAATGGCTTATGGAAT 134022
QY 901 TGTGTTTGTGCGCTTAG 918
Db 134023 TGTGTTTGTGCGCTTAG 134040

RESULT 13
AX453412
LOCUS AX453412 1051 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 1 from Patent WO0244212.
ACCESSION AX453412
VERSION AX453412.1 GI:21712725
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
Deleersnijder W., Blockx, H. and de Moor, L.
Human g-protein coupled receptor and uses thereof
Patent: WO 0244212-A 1 06-JUN-2002;
SOLVAY PHARMACEUTICALS B V (NL)
FEATURES
Location/Qualifiers
1..1051
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
60..977
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD38106.1"
/db_xref="GI:21712725"
/db_xref="REMBL:CAD38106"
/translation="MPGHTSRNSGSDIVTPHLSIFVILIGLVGVISILFLVK
MNTSRVTTMAYINLVVHVSFLVLPFLYLIKKTWMPGLPFCFKFVSAMLIHMYLT
FLFYVILVTRYLIPFKCKQVFEYRKLHVAASAGMWTLIVIVLWPLVSRVGIHEE
YNEHCFFKFKELAYTVYVKIINYMIVIFVIAVAVILLVQVFIIMLVQKLRHLLSH

CDS

QEFWAQXNLFFIGVILVCELPYQFFRIYLYNVVTHSNACNSKVAFYNEIFLSVTAIS
CYDLLLFFVGGSHWFKKIIGLWNCVLCR"
ORIGIN
Query Match 99.8%; Score 916.4; DB 6; Length 1051;
Best Local Similarity 99.9%; Pred. No. 4.6e-225;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCTCGGCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
Db 60 ATGCTCGGCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 119
QY 61 ATGAGCTCTACTTCATAGTGTCTTATGGCGGGCTGTGGGTGTCATTTCCATTCCTTTTC 120
Db 120 ATGAGCTCTACTTCATAGTGTCTTATGGCGGGCTGTGGGTGTCATTTCCATTCCTTTTC 179
QY 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAATGCGGGTCACTTAACCTTGGTGGTG 180
Db 180 CTCCTGTGAAATGAACACCCGGTCACTGACCAATGCGGGTCACTTAACCTTGGTGGTG 239
QY 181 GTCACAGCGTTTTCGTGACAGTGCCATTTGCTTGACCTACCTCATCAAGAAGACT 240
Db 240 GTCACAGCGTTTTCGTGACAGTGCCATTTGCTTGACCTACCTCATCAAGAAGACT 299
QY 241 TGGATGTTGGGCTGCCCTTCGCAATTTGTGAGTGCCATGTCACATCCCATGTAC 300
Db 300 TGGATGTTGGGCTGCCCTTCGCAATTTGTGAGTGCCATGTCACATCCCATGTAC 359
QY 301 CTCACGTTCTATTTATGTTGATCCTGGTCAACAGATACCTCATCTTCTTCAAGTGC 360
Db 360 CTCACGTTCTATTTATGTTGATCCTGGTCAACAGATACCTCATCTTCTTCAAGTGC 419
QY 361 AAGACAAAGTGGAAATCTACAGAAATCTGCTGTGGCTGCCAGTCTGGCATGGG 420
Db 420 AAGACAAAGTGGAAATCTACAGAAATCTGCTGTGGCTGCCAGTCTGGCATGGG 479
QY 421 ACGCTGTGATTTGTCATTTGTTGATACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480
Db 480 ACGCTGTGATTTGTCATTTGTTGATACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 539
QY 481 TACAATGAGGAGCAGCTGTTTAAATTTACAAAGAGCTTGTCTTACATATGTGAAATC 540
Db 540 TACAATGAGGAGCAGCTGTTTAAATTTACAAAGAGCTTGTCTTACATATGTGAAATC 599
QY 541 ATCAACTATATGATGATGATTTTGTGATGAGCGCTTGTGATGCTGTGCTTCCAG 600
Db 600 ATCAACTATATGATGATGATTTTGTGATGAGCGCTTGTGATGCTGTGCTTCCAG 659
QY 601 GTCCTCATCATTTATGTTGATGTTGAGAGCTACGCCACTCTTTACTATCCACACAGAG 660
Db 660 GTCCTCATCATTTATGTTGATGTTGAGAGCTACGCCACTCTTTACTATCCACACAGAG 719
QY 661 TTTGGGCTCAGCTGAAACCTATTTTATAGGGTGTATCCCTTTGTTGTTTCTTCCC 720
Db 720 TTTGGGCTCAGCTGAAACCTATTTTATAGGGTGTATCCCTTTGTTGTTTCTTCCC 779
QY 721 TACCAGTCTTTAGGATCTATTTACTTGAATGTTGTCAGCAATTCCTGCTGTAAACAGC 780
Db 780 TACCAGTCTTTAGGATCTATTTACTTGAATGTTGTCAGCAATTCCTGCTGTAAACAGC 839
QY 781 AAGGTTGCAATTTTAAACCAATCTTTGAGTGTAAACAGCAATTAGCTGTATGATTG 840
Db 840 AAGGTTGCAATTTTAAACCAATCTTTGAGTGTAAACAGCAATTAGCTGTATGATTG 899
QY 841 CTTCTCTTTGCTTTGGGGAGGCAATGTTTAAACCAAGATTAATGGCTTATGGAAT 900
Db 900 CTTCTCTTTGCTTTGGGGAGGCAATGTTTAAACCAAGATTAATGGCTTATGGAAT 959
QY 901 TGTGTTTGTGCGCTTAG 918
Db 960 TGTGTTTGTGCGCTTAG 977

8696	8979	764	755	3414	3439	956	988	4946	4869	14	<800
6	<800	6382	6611	2067	2102	2026	2123	6247	6163	44	<800
663	<800	512	<800	5356	5585	1821	1788	685	<800	10402	10380
122	<800	449	<800	1416	1421	2453	2471	1367	1406	300	<800
174	<800	1059	1063	610	<800	8955	9499	109	<800	5150	5294
4551	4612	70	<800	225	<800	1004	988	3608	3535	3195	3246
952	988	424	<800	932	961	7399	7468	7728	7736	2281	2309
968	988	2594	2670	1982	2102	7516	7468	4264	4301	2740	2804
980	988	3852	3908	29	<800	4119	4107	357	<800	5869	5921
10043	10231	915	918	2663	2719	193	<800	3645	3709	248	<800
2412	2471	5333	5315	5958	5921	2792	2805	1961	2031	3072	3079
3670	3625	4795	4869	448	<800	7034	7468	5668	5598	585	<800
4365	4323	668	<800	8190	8084	4940	4902	957	918	655	<800
27	<800	552	<800	1869	1948	603	<800	5024	4869	1206	1270
9749	10231	1010	1063	3655	3640	761	<800	201	<800	1723	1693
703	<800	884	918	14842	14314	2518	2471	1119	1195	19721	20141
1957	2017	2280	2278	3924	3962	4086	4107	709	<800	2331	2309
2403	2471	4595	4869	591	<800	5916	5835	4907	4869	1940	1993
9	<800	654	<800	1362	1270	6995	6947	1161	1195	5574	5585
359	<800	2624	2670	572	<800	4667	4612	11292	11329	3867	3865
57	<800	13428	13500	2139	2102	10434	10231	6699	6611	1268	1270
2128	2184	12540	12591	1593	1527	1306	1313	1358	1406	8347	8084
1087	1101	4819	4869	2049	2102	374	<800	2400	2394	3636	3640
2839	2805	11280	11329	614	<800	Query Match 100.0%; Score 918; DB 9; Length 218186; Best Local Similarity 100.0%; Pred. No. 3.le-225; Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
2787	2805	840	918	7901	8084	QY 1 ATGCTGGCCACATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCACTTA 60					
5407	5309	9244	8985	619	<800	DB 133123 ATGCTGGCCACATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCACTTA 133182					
3324	3348	1672	1707	5583	5585	QY 61 ATCAGCCTCTACTTCATAGTCTTATTGGGGGGTGGTGGTGCATTTCCTTCCTTTTC 120					
7246	7468	3195	3163	345	<800	DB 133183 ATCAGCCTCTACTTCATAGTCTTATTGGGGGGTGGTGGTGCATTTCCTTCCTTTTC 133242					
4508	4455	4273	4301	324	<800	QY 121 CTCCTGGTGAATAACACCCCGTCACTGACCACTGGCGGTCACTTAATCTGGTGGTG 180					
5815	5686	1980	2031	1496	1421	DB 133243 CTCCTGGTGAATAACACCCCGTCACTGACCACTGGCGGTCACTTAATCTGGTGGTG 133302					
5380	5309	520	<800	6710	6637	QY 181 GTCCACAGCGTTTTCTGCTGACAGTGCCTTCGCTTGACCTACCTCATCAAGAAGACT 240					
349	<800	737	755	71	<800	DB 133303 GTCCACAGCGTTTTCTGCTGACAGTGCCTTCGCTTGACCTACCTCATCAAGAAGACT 133362					
4509	4612	1833	1878	848	877	QY 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGTCGACATCCATGATAC 300					
571	<800	8798	8985	6153	6135	DB 133363 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGTCGACATCCATGATAC 133422					
4162	4455	2024	2031	4085	4113	QY 301 CTCAGGTTCTTCTATGTTGTTGATCTCTGCTCACCAGATACCTCATCTTCTCAAGTGC 360					
						DB 133423 CTCAGGTTCTTCTATGTTGTTGATCTCTGCTCACCAGATACCTCATCTTCTCAAGTGC 133482					

```
QY 61 ATAGCCTCTACTTCATAGTGTCTATTATGGCGGCTGGTGGGTGTCATTTCCATCTTTTC 120
Db 11600 ATCAGCCTCTACTTCATAGTGTCTATTATGGCGGCTGGTGGGTGTCATTTCCATCTTTTC 11659
QY 121 CTCTGCTGAAATGAACACCCGTCAGTCACACCATGCGGTGTCATTAACTTGGTGGTG 180
Db 11660 CTCTGCTGAAATGAACACCCGTCAGTCACACCATGCGGTGTCATTAACTTGGTGGTG 11719
QY 181 GTCACAGCGCTTTTCTGCTGACAGTGCCATTTGCTTGACCTTACCTTCAAGAAAGACT 240
Db 11720 GTCACAGCGCTTTTCTGCTGACAGTGCCATTTGCTTGACCTTACCTTCAAGAAAGACT 11779
QY 241 TGGATGTTTGGGCTGCCCTCTGCAATTTGTCAGTGCCATGCTGCACATCCCATGTAC 300
Db 11780 TGGATGTTTGGGCTGCCCTCTGCAATTTGTCAGTGCCATGCTGCACATCCCATGTAC 11839
QY 301 CTCACGTTCTCTATTCTATGTTGGTGATCTCTGTCACACAGATACCTCATCTTCTCAAGTGC 360
Db 11840 CTCACGTTCTCTATTCTATGTTGGTGATCTCTGTCACACAGATACCTCATCTTCTCAAGTGC 11899
QY 361 AAGACAAAGTGAATCTACAGAACTGCATGCTGTGGCTGCCAGTCTGCCATGTGG 420
Db 11900 AAGACAAAGTGAATCTACAGAACTGCATGCTGTGGCTGCCAGTCTGCCATGTGG 11959
QY 421 ACCTGCTGATTCATTTGTTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480
Db 11960 ACCTGCTGATTCATTTGTTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 12019
QY 481 TACAATGAGGAGCAGCTTTTAAATTTACAAAGAGCTTGCTTACATATGTGAAATC 540
Db 12020 TACAATGAGGAGCAGCTTTTAAATTTACAAAGAGCTTGCTTACATATGTGAAATC 12079
QY 541 ATCAACTATATGATGATGCTATTTTGTGATAGCGGTTGCTGATTCCTGTGCTTCCAG 600
Db 12080 ATCAACTATATGATGATGCTATTTTGTGATAGCGGTTGCTGATTCCTGTGCTTCCAG 12139
QY 601 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACAGGAG 660
Db 12140 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACAGGAG 12199
QY 661 TTCTGGGCTCAGTGAAAACTATTTTATAGGGGTGTCATCTTGTGTTCTTCTCC 720
Db 12200 TTCTGGGCTCAGTGAAAACTATTTTATAGGGGTGTCATCTTGTGTTCTTCTCC 12259
QY 721 TACCACTCTTTAGGATCTATTACTTGAATTTGTGACCATTCACATGCTGTAACAGC 780
Db 12260 TACCACTCTTTAGGATCTATTACTTGAATTTGTGACCATTCACATGCTGTAACAGC 12319
QY 781 AAGGTTGCAATTTATACCAATCTCTGATGTAACAGCAATTAGCTGCTATGTTG 840
Db 12320 AAGGTTGCAATTTATACCAATCTCTGATGTAACAGCAATTAGCTGCTATGTTG 12379
QY 841 CTCTCTTTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAATGGCTTATGGAA 900
Db 12380 CTCTCTTTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAATGGCTTATGGAA 12439
QY 901 TGTGTTTGTGGCTAG 918
Db 12440 TGTGTTTGTGGCTAG 12457
```

RESULT 12

```
AC083865
LOCUS AC083865 218186 bp DNA linear PRI 26-JAN-2001
DEFINITION Homo sapiens chromosome 7 clone RP11-605P22, complete sequence.
ACCESSION AC083865
VERSION AC083865.2 GI:12545315
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```
1 (bases 1 to 218186)
Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
Olson,M.V.
Large-scale Mapping and Sequencing of Human Chromosome 7
Unpublished
2 (bases 1 to 218186)
Kaul,R., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.
Direct Submission
Submitted (04-OCT-2000) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 218186)
Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
Olson,M.V.
Direct Submission
Submitted (28-JAN-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jan 26, 2001 this sequence version replaced gi:10567930.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgc@gsu.washington.edu
----- Project Information
Center project name: HsaChr7
Center clone name: RP11-605P22 (djs708)
----- Summary Statistics
Sequencing vector: plasmid; X52328; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 217693 bases at least Q40
Consensus quality: 218145 bases at least Q30
Consensus quality: 218186 bases at least Q20
Insert size: 273875; 19.1% error; agarose-fp
Insert size: 218186; sum-of-contigs
Quality coverage: 8.30x in Q20 bases; agarose-fp
Quality coverage: 10.42x in Q20 bases; sum-of-contigs
-----
```

Overlapping Sequences:

```
5': mapping in progress
3': RP11-243E12 (UMGC:djs156) AC018634, 6468-bp overlap
-----
```

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI HindIII BglII

SeqDerMap FngPrnt SeqDerMap FngPrnt SeqDerMap FngPrnt

```

Db      867  CTTCTCTTTGCTTTGGGGAAGCCATTCGTTTAAAGCAAAAGATAAATGGCTTATGGAAT 926
QY      901  TGTGTTTTCGCGGTAG 918
Db      927  TGTGTTTTCGCGGTAG 944

RESULT 10
AX521885      2525 bp      DNA      linear      PAT 24-OCT-2002
LOCUS      Sequence 81 from Patent WO02064789.
DEFINITION  AX521885
ACCESSION  AX521885
VERSION    AX521885.1  GI:24410791
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Lind, P.; Parodi, L.A.; Vogeli, G. and Wood, L.S.
TITLE     G protein-coupled receptor
JOURNAL   Patent: WO 02064789-A 81 22-AUG-2002;
           PHARMACIA & UPJOHN COMPANY (US)
FEATURES   Location/Qualifiers
           1..2525
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 918; DB 6; Length 2525;
Best Local Similarity 100.0%; Pred. No. 1.9e-225;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGCTGGGCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACCCCACTTA 60
Db      27  ATGCTGGGCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACCCCACTTA 86
QY      61  ATCAGCTCTACTTCTATAGTGTCTTATGGCGGCTGGTGGTGTCAATTTCCATTTCTTTTC 120
Db      87  ATCAGCTCTACTTCTATAGTGTCTTATGGCGGCTGGTGGTGTCAATTTCCATTTCTTTTC 146
QY      121 CTCTCTGGTGAATAGAACCCCGTCAAGTGCACCATGCGGTCAATTAACCTGGTGGTG 180
Db      147 CTCTCTGGTGAATAGAACCCCGTCAAGTGCACCATGCGGTCAATTAACCTGGTGGTG 206
QY      181 GTCCACAGCGTTTCTCTGTCAGTGCACATTTTCGCTTACCTACCTCATCAAGAAGACT 240
Db      207 GTCCACAGCGTTTCTCTGTCAGTGCACATTTTCGCTTACCTCATCAAGAAGACT 266
QY      241 TGGATGTTGGGCTGCGCTTCTGCAATTTGTGAGTGCCCATGTCGACATCCACATGTAC 300
Db      267 TGGATGTTGGGCTGCGCTTCTGCAATTTGTGAGTGCCCATGTCGACATCCACATGTAC 326
QY      301 CTCACGTTCTATCTATGTTGGTGATCCTGGTGCACAGATACCTCATCTTCTTCAAGTGC 360
Db      327 CTCACGTTCTATCTATGTTGGTGATCCTGGTGCACAGATACCTCATCTTCTTCAAGTGC 386
QY      361 AAAGACAAAGTGAATCTTACAGAAATCTCATGCTGTGGCTGCCAGTGTGTCATGTGG 420
Db      387 AAAGACAAAGTGAATCTTACAGAAATCTCATGCTGTGGCTGCCAGTGTGTCATGTGG 446
QY      421 ACCTGTGTGATGTCATGTTGGTACCCCTGTTGTCTCCCGGTATGGAATCCATGAGGA 480
Db      447 ACCTGTGTGATGTCATGTTGGTACCCCTGTTGTCTCCCGGTATGGAATCCATGAGGA 506
QY      481 TACAATGAGGAGACACTGTTTAAATTTCAAGAGAGCTTCTTTACACATATGTGAAATC 540
Db      507 TACAATGAGGAGACACTGTTTAAATTTCAAGAGAGCTTCTTTACACATATGTGAAATC 566
QY      541 ATCAACTATATGATGATCAATTTTGTGCATAGCCGTTGTCTGTGATTCCTGTGCTTCCAG 600
Db      567 ATCAACTATATGATGATCAATTTTGTGCATAGCCGTTGTCTGTGATTCCTGTGCTTCCAG 626

```

```

QY      601  GTCTTCATCATATGTTGATGTTGCGAAGACTACGCACCTTCTTACTATATCCACACAGGAG 660
Db      627  GTCTTCATCATATGTTGATGTTGCGAAGACTACGCACCTTCTTACTATATCCACACAGGAG 686
QY      661  TTCTGGGCTCAGCTGAAAAACCTATTTTATATAGGGGTTCATCTTGTGTTTCTTCTTCCC 720
Db      687  TTCTGGGCTCAGCTGAAAAACCTATTTTATATAGGGGTTCATCTTGTGTTTCTTCTTCCC 746
QY      721  TACCAGTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCCTGCTGTAACAGC 780
Db      747  TACCAGTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCCTGCTGTAACAGC 806
QY      781  AAGTTTGCATTTTATACGAAATCTTCTTGAGTGTAAACAGCAATTAGCTCTATGATTG 840
Db      807  AAGTTTGCATTTTATACGAAATCTTCTTGAGTGTAAACAGCAATTAGCTCTATGATTG 866
QY      841  CTTCTCTTTTGTCTTTGGGGAAGCATTTGTTTAAAGCAAAAGATAATTTGCTTATGGAAT 900
Db      867  CTTCTCTTTTGTCTTTGGGGAAGCATTTGTTTAAAGCAAAAGATAATTTGCTTATGGAAT 926
QY      901  TGTGTTTTCGCGGTAG 918
Db      927  TGTGTTTTCGCGGTAG 944

RESULT 11
AX646815      113306 bp      DNA      linear      PAT 04-MAR-2003
LOCUS      Sequence 1007 from Patent EP1270724.
DEFINITION  AX646815
ACCESSION  AX646815.1  GI:28799225
VERSION    AX646815.1  GI:28799225
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
TITLE     Guanosine triphosphate-binding protein coupled receptors
JOURNAL   Patent: EP 1270724-A 1007 02-JAN-2003;
           National Institute of Advanced Industrial Science and Technology
           (JP); Center for Advanced Science and Technology Incubation, Ltd.
           (JP)
FEATURES   Location/Qualifiers
           1..113306
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            join(201..207,11526..12452,37954..38097,98732..98784,
            112891..113106)
            /note="unnamed protein product"
            /codon_start=1
            /protein_id="CAD69533.1"
            /db_xref="GI:28799226"
            /translation="MTGDFSPMGHNTSRNSGDPVTPHLISLYFIVLIGLVGLVIS
            ILFLVKNRSTVTMAVILNVVSVLPTVPERLTLTKMTMGLPCKFVSAML
            HHMTLPLFVVLVTRYLIFFCKDKVEFKLHAVAASAGNWTIVIVLPLVUS
            RYGHSEYNEHCFFKHELAITYKLIINTMIVIFVIAVAIVLLVQVFIIMLVQKL
            RSHLSHQEFWAQKNLFFGVLVLCFLPYOFFRIYLVNVVTHSNACNSKVAFFNEIF
            LSVTAISQDILLFVFGGSHWFKQKIGLWNCVLCRNSPGLTFCFSQLSLFLPLPAM
            AGSGVHCSVLRIGEVSEKCFFLRHFTDLCLMFFNHHTYAKVFERSVTKLESGTI
            SAHCTLYLPDSSNSPASQVAGITGTTHHAQLIFVFLVETGPHVHGQDGLDLTSL"

CDS
Query Match      100.0%; Score 918; DB 6; Length 113306;
Best Local Similarity 100.0%; Pred. No. 2.9e-225;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGCTGGGCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACCCCACTTA 60
Db      11540 ATGCTGGGCAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACCCCACTTA 11599

```

Db 403 ATCAGCCTCTACTTTCATAGTGTCTATTGGCGGGTGGTGGTGTGATCTTCCATCTTTTC 462
Qy 121 CTCCTGGTGAATAAGAACACCCGGTCACTGACACACCATGGCGGTCTATTAACCTTGGTGTG 180
Db 463 CTCCTGGTGAATAAGAACACCCGGTCACTGACACACCATGGCGGTCTATTAACCTTGGTGTG 522
Qy 181 GTCCACAGCGTTTCTCTGCTGACAGTGCATTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 240
Db 523 GTCCACAGCGTTTCTCTGCTGACAGTGCATTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 582
Qy 241 TGGATGTTTGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 583 TGGATGTTTGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642
Qy 301 CTCAGCTTCTTCTATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 643 CTCAGCTTCTTCTATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
Qy 361 AAAGCAAGTGAATTTACAGAAACTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 703 AAAGCAAGTGAATTTACAGAAACTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
Qy 421 AGCTGGTGTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 763 AGCTGGTGTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
Qy 481 TACATGAGGAGCACTGTTTAAATTTACAAAGAGCTTGTCTTACATATGTGAAATC 540
Db 823 TACATGAGGAGCACTGTTTAAATTTACAAAGAGCTTGTCTTACATATGTGAAATC 882
Qy 541 ATCAACTATATGATGCTATTTTGTGCTAGCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 883 ATCAACTATATGATGCTATTTTGTGCTAGCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 942
Qy 601 GTCTTCATCATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 943 GTCTTCATCATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1002
Qy 661 TTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 1003 TTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1062
Qy 721 TACCAAGTCTTTAGGATCTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 1063 TACCAAGTCTTTAGGATCTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1122
Qy 781 AAGGTGCTATTTTAAAGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 1123 AAGGTGCTATTTTAAAGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
Qy 841 CTCTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 1183 CTCTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1242
Qy 901 TGTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 1243 TGTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260

RESULT 9
AX147836
LOCUS AX147836 2525 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 81 from Patent WO0136473.
ACCESSION AX147836
VERSION AX147836.1 GI:14346839
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Vogeli, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P.,
Slightom, J., Schellin, K.A., Kaytes, P.S., Bannigan, C.M., Ruff, V.,

Sejltiz, T. and Huff, R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 81 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
source Location/Qualifiers
1. 2525
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 2525;
Best Local Similarity 100.0%; Pred. No. 1.9e-225;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTGGATCCTATAGTGACACCCCACTTA 60
Db 27 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTGGATCCTATAGTGACACCCCACTTA 86
Qy 61 ATGAGCTCTACCTTCACTAGTCTTATGGCGGCTGGTGGTGTCAATTCCTTTC 120
Db 87 ATGAGCTCTACCTTCACTAGTCTTATGGCGGCTGGTGGTGTCAATTCCTTTC 146
Qy 121 CTCTGCTGAAATGAACACCCGCTCAGTGACACCACTGCGGTCAATTAACCTTGGTGGTG 180
Db 147 CTCTGCTGAAATGAACACCCGCTCAGTGACACCACTGCGGTCAATTAACCTTGGTGGTG 206
Qy 181 GTCCACAGCGTTTCTGCTGACAGTCCCAATTCGCTTGAACCTTCACTCAAGAAAGACT 240
Db 207 GTCCACAGCGTTTCTGCTGACAGTCCCAATTCGCTTGAACCTTCACTCAAGAAAGACT 266
Qy 241 TGGATGTTGGGCTGCGCTTCTGCAAAATTTGTAGTGCCATGCTGACACATCCACATGTAC 300
Db 267 TGGATGTTGGGCTGCGCTTCTGCAAAATTTGTAGTGCCATGCTGACACATCCACATGTAC 326
Qy 301 CTCAAGTTCCTATTTCTATGTTGGTGAATTCCTGCTGACAGTACCTTCTTCTTCAAGTGC 360
Db 327 CTCAAGTTCCTATTTCTATGTTGGTGAATTCCTGCTGACAGTACCTTCTTCTTCAAGTGC 386
Qy 361 AAAGCAAGTGAATTTACAGAAACTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 387 AAAGCAAGTGAATTTACAGAAACTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 446
Qy 421 AGCTGGTGTATGCTATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 447 AGCTGGTGTATGCTATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506
Qy 481 TACATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGAAATC 540
Db 507 TACATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGAAATC 566
Qy 541 ATCAACTATATGATGCTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 567 ATCAACTATATGATGCTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 626
Qy 601 GTCTTCATCATTTATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 627 GTCTTCATCATTTATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 686
Qy 661 TTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 687 TTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 746
Qy 721 TACAGTTCCTTTAGGATCTATTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 747 TACAGTTCCTTTAGGATCTATTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806
Qy 781 AAGTTGCAATTTTAAAGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 807 AAGTTGCAATTTTAAAGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 866
Qy 841 CTCTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

QY 841 CTTCTCTTTGTTGGGGGAGCCATTGGTTTAAAGCAAGATAATTGGCTTATGGAAT 900
Db 1059 CTTCTCTTTGTTGGGGGAGCCATTGGTTTAAAGCAAGATAATTGGCTTATGGAAT 1118

QY 901 TGTGTTTTGTCGGTTAG 918
Db 1119 TGTGTTTTGTCGGTTAG 1136

RESULT 7
LOCUS AX709194 1340 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 53 from Patent WO02063004.
ACCESSION AX709194
VERSION AX709194.1 GI:29564788
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallik, D.A., Gandhi, A.R., Wallia, N.K., Arvizu, C., Elliott, V.S.,
Hafalia, A.J., Runkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Graul, R.C., Khan, P.A., Walsh, R.T., Ison, C.H.,
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and
Harland, L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 02063004-A 53 15-AUG-2002;
Incyte Genomics, Inc. (US)
FEATURES
source Location/Qualifiers
1. 1340
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 90012586CB1"

ORIGIN
Query Match 100.0%; Score 918; DB 6; Length 1340;
Best Local Similarity 100.0%; Pred. No. 1.8e-225; Indels 0; Gaps 0;
Matches 918; Conservative 0; Mismatches 0

QY 1 ATGCCTGGCCACATACCTCCAGGAATTCCTTGGCATCTATAGTGACACCCCACTTA 60
Db 223 ATGCCTGGCCACATACCTCCAGGAATTCCTTGGCATCTATAGTGACACCCCACTTA 282

QY 61 ATCAGCCTCTACTCTATAGTGCTTATTTGGGGGCTGGTGGTGCATTTCCATCTTTTC 120
Db 283 ATCAGCCTCTACTCTATAGTGCTTATTTGGGGGCTGGTGGTGCATTTCCATCTTTTC 342

QY 121 CTCCTGGTGAATGAACACCCGGTCAGTGACACCATGGCGGTCTTAACTTTGGTGGTG 180
Db 343 CTCCTGGTGAATGAACACCCGGTCAGTGACACCATGGCGGTCTTAACTTTGGTGGTG 402

QY 181 GTCCACAGCGTTTTCTGTGACAGTGCCATTTTCGTTGACCTCTCATCAAGAGACT 240
Db 403 GTCCACAGCGTTTTCTGTGACAGTGCCATTTTCGTTGACCTCTCATCAAGAGACT 462

QY 241 TGGATGTTTGGCTGCCCTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
Db 463 TGGATGTTTGGCTGCCCTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 522

QY 301 CTCACGTTCTCTATTTCTATGTTGGTGTATCTGTGTACACCATCTCTCTTCTCAAGTGC 360
Db 523 CTCACGTTCTCTATTTCTATGTTGGTGTATCTGTGTACACCATCTCTCTTCTCAAGTGC 582

QY 361 AAAGACAAGTGGAAATTTACAGAAATCTGATCTGTGGTGCAGTGTGGCATGTGG 420
Db 583 AAAGACAAGTGGAAATTTACAGAAATCTGATCTGTGGTGCAGTGTGGCATGTGG 642

QY 421 ACGCTGGTGAATGTCTATGTTGGTACCCCTGTTGTCTCCCGGTATGGAATCCATGAGAA 480
Db 643 ACGCTGGTGAATGTCTATGTTGGTACCCCTGTTGTCTCCCGGTATGGAATCCATGAGAA 702

QY 481 TACAATGAGGAGCAGCTGTTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAATC 540
Db 703 TACAATGAGGAGCAGCTGTTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAATC 762

QY 541 ATCAACTATATGATAGTCAATTTTGTGCATAGCCGTTGCTGTGATTCCTGTTGGTCTTCCAG 600
Db 763 ATCAACTATATGATAGTCAATTTTGTGCATAGCCGTTGCTGTGATTCCTGTTGGTCTTCCAG 822

QY 601 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTTACTATCCCAACAGGAG 660
Db 823 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTTACTATCCCAACAGGAG 882

QY 661 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTGCATCCTGTTGTTGTTCTTCCCTCCC 720
Db 883 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTGCATCCTGTTGTTGTTCTTCCCTCCC 942

QY 721 TACCAGTTCCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCTCAATGCTGTAAACAGC 780
Db 943 TACCAGTTCCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCTCAATGCTGTAAACAGC 1002

QY 781 AAGGTTGATTTTATAACGAAATCTTCTTGAGTGTACAGCAATTAGCTGCTATGATTG 840
Db 1003 AAGGTTGATTTTATAACGAAATCTTCTTGAGTGTAAACGCAATTAGCTGCTATGATTG 1062

QY 841 CTTCTCTTTGCTTTGGGGGAGCCATTGGTTTAAAGCAAGATAATTGGCTTATGGAAT 900
Db 1063 CTTCTCTTTGCTTTGGGGGAGCCATTGGTTTAAAGCAAGATAATTGGCTTATGGAAT 1122

QY 901 TGTGTTTTGTCGGTTAG 918
Db 1123 TGTGTTTTGTCGGTTAG 1140

RESULT 8
LOCUS AX709195 1460 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 54 from Patent WO02063004.
ACCESSION AX709195
VERSION AX709195.1 GI:29564789
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallik, D.A., Gandhi, A.R., Wallia, N.K., Arvizu, C., Elliott, V.S.,
Hafalia, A.J., Runkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Graul, R.C., Khan, P.A., Walsh, R.T., Ison, C.H.,
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and
Harland, L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 02063004-A 54 15-AUG-2002;
Incyte Genomics, Inc. (US)
FEATURES
source Location/Qualifiers
1. 1460
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 90012670CB1"

ORIGIN
Query Match 100.0%; Score 918; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 1.8e-225; Indels 0; Gaps 0;
Matches 918; Conservative 0; Mismatches 0

QY 1 ATGCCTGGCCACATACCTCCAGGAATTCCTTGGCATCTATAGTGACACCCCACTTA 60
Db 343 ATGCCTGGCCACATACCTCCAGGAATTCCTTGGCATCTATAGTGACACCCCACTTA 402

QY 61 ATCAGCCTCTACTCTATAGTGCTTATTTGGGGGCTGGTGGTGCATTTCCATCTTTTC 120

121 CTCCTGGTGAATGAACACCCGGTCACTGACCACTGGGGTCACTTAACCTGGTGGT 180
Db CTCCTGGTGAATGAACACCCGGTCACTGACCACTGGGGTCACTTAACCTGGTGGT 180
181 GTCCACAGCGTTTCTCTGACAGTGCATTTGGCTGACCTACCTCATCAAGAGACT 240
Db GTCCACAGCGTTTCTCTGACAGTGCATTTGGCTGACCTACCTCATCAAGAGACT 240
241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGGAGTGCCTGCAATCCATCCATGTAC 300
Db TGGATGTTGGGCTGCCCTTCTGCAAAATTTGGAGTGCCTGCAATCCATCCATGTAC 300
301 CTCACGTTCCCTATCTATGCTGTGATCCTGTCACCAAGATACCTCATCTTCAAGTGC 360
Db CTCACGTTCCCTATCTATGCTGTGATCCTGTCACCAAGATACCTCATCTTCAAGTGC 360
361 AAAGCAAAAGTGGAAATCTACAGAAATCTGATGCTGGCTGCCAGTGGCATGGTGG 420
Db AAAGCAAAAGTGGAAATCTACAGAAATCTGATGCTGGCTGCCAGTGGCATGGTGG 420
421 ACGCTGGTGAATGTCATTTGCTGTGATCCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db ACGCTGGTGAATGTCATTTGCTGTGATCCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
481 TACAATGAGGACCTGTTTAAATTTCAAAAGAGCTGCTTACACATATGTGAATC 540
Db TACAATGAGGACCTGTTTAAATTTCAAAAGAGCTGCTTACACATATGTGAATC 540
541 ATCAACTATATGATAGTCAATTTGCTATGAGCGTGTGCTGATCTGCTGCTTCCAG 600
Db ATCAACTATATGATAGTCAATTTGCTATGAGCGTGTGCTGATCTGCTGCTTCCAG 600
601 GTCTTCATCATTTATGATGAGTGCAGAGCTACGCCACTCTTACTATCCACAGGAG 660
Db GTCTTCATCATTTATGATGAGTGCAGAGCTACGCCACTCTTACTATCCACAGGAG 660
661 TTCTGGGCTCAGCTGAAGAACTATTTTATAGGGTCACTCTTGTGTTGTTCTTCCC 720
Db TTCTGGGCTCAGCTGAAGAACTATTTTATAGGGTCACTCTTGTGTTGTTCTTCCC 720
721 TACCAGTCTTTAGGATCTATTCTGTAATGTTGTGAGCAATCCAAATGCCGTGAACAG 780
Db TACCAGTCTTTAGGATCTATTCTGTAATGTTGTGAGCAATCCAAATGCCGTGAACAG 780
781 AAGGTGCAATTTTAAACGAATCTTCTGAGTGAACAGCAATAGCTGCTATGATTTG 840
Db AAGGTGCAATTTTAAACGAATCTTCTGAGTGAACAGCAATAGCTGCTATGATTTG 840
841 CTCTCTTTGTTCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTGGCTTATGGA 900
Db CTCTCTTTGTTCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTGGCTTATGGA 900
901 TGTGTTTGTGCGGTTAG 918
Db TGTGTTTGTGCGGTTAG 918

RESULT 6
AX709193
LOCUS AX709193 1336 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 52 from Patent WO02063004.
ACCESSION AX709193
VERSION AX709193.1 GI:29564787
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
AUTHORS Kallick, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S.,
Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,

Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and Harland, L.
G-protein coupled receptors
Patent: WO 02063004-A 52 15-AUG-2002;
Incyte Genomics, Inc. (US)
FEATURES
Location/Qualifiers
1..1336
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 90012430CB1"
ORIGIN
Query Match 100.0%; Score 918; DB 6; Length 1336;
Best Local Similarity 100.0%; Pred. No. 1.8e-225; Indels 0; Gaps 0;
Matches 918; Conservative 0; Mismatches 0;
QY 1 ATCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTAGACACCCCACTTA 60
Db 219 ATCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTAGACACCCCACTTA 278
QY 61 ATCAGCCTCTATCTTATAGTCTTATTTGGGGGCTGGTGGTGTCTATTTCCATCTTTTC 120
Db 279 ATCAGCCTCTATCTTATAGTCTTATTTGGGGGCTGGTGGTGTCTATTTCCATCTTTTC 338
QY 121 CTCTGGTGAATGAACACCCGGTCACTGACCACTGCGGTCACTTAACCTTGGTGGT 180
Db 339 CTCTGGTGAATGAACACCCGGTCACTGACCACTGCGGTCACTTAACCTTGGTGGT 398
181 GTCCACAGCGTTTCTGCTGACAGTGCCTATTTGCTTGAACCTCATCTCAAGAGACT 240
Db 399 GTCCACAGCGTTTCTGCTGACAGTGCCTATTTGCTTGAACCTCATCTCAAGAGACT 458
241 TGAATGTTGGGCTGCCCTTCTGCAAAATTTGTCAGTGCCTATGTCACATCCACATGTAC 300
Db 459 TGAATGTTGGGCTGCCCTTCTGCAAAATTTGTCAGTGCCTATGTCACATCCACATGTAC 518
301 CTCAAGTTCCTATTTCTATGTTGATCCTGCTCACCAGATACCTCATCTTCTTCAAGTGC 360
Db 519 CTCAAGTTCCTATTTCTATGTTGATCCTGCTCACCAGATACCTCATCTTCTTCAAGTGC 578
361 AAAGCAAAAGTGGAAATCTACAGAAATCTGATGCTGGCTGCCAGTGGCATGGTGG 420
Db 579 AAAGCAAAAGTGGAAATCTACAGAAATCTGATGCTGGCTGCCAGTGGCATGGTGG 638
421 ACGCTGGTGAATGTCATTTGTCACCCCTGGTGTCTCTCCGGTATGGAATCCATGAGGAA 480
Db 639 ACGCTGGTGAATGTCATTTGTCACCCCTGGTGTCTCTCCGGTATGGAATCCATGAGGAA 698
481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAATC 540
Db 699 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTGTACACATATGTGAATC 758
541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATTTCTGTTGGTCTTCCAG 600
Db 759 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATTTCTGTTGGTCTTCCAG 818
601 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTATATCCACAGGAG 660
Db 819 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTATATCCACAGGAG 878
661 TTCTGGGCTCAGCTGAAGAACTATTTTATAGGGGCTCATCTTGTGTTGTTCTTCCC 720
Db 879 TTCTGGGCTCAGCTGAAGAACTATTTTATAGGGGCTCATCTTGTGTTGTTCTTCCC 938
721 TACCAGTTCCTTAGGATCTATTCTTGAATGTTGTGACGCAATCCAAATGCCGTGAACAGC 780
Db 939 TACCAGTTCCTTAGGATCTATTCTTGAATGTTGTGACGCAATCCAAATGCCGTGAACAGC 998
781 AAGGTGCAATTTTAAACGAATCTTCTTGAATGTTGAACAGCAATAGCTGCTATGATTTG 840
Db 999 AAGGTGCAATTTTAAACGAATCTTCTTGAATGTTGAACAGCAATAGCTGCTATGATTTG 1058

Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and Harland, L.
G-protein coupled receptors
Patent: WO 02063004-A 52 15-AUG-2002;
Incyte Genomics, Inc. (US)
FEATURES
Location/Qualifiers
1..1336
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 90012430CB1"

Novel Polypeptide
Patent: JP 2003024082-A 1 28-JAN-2003;
Pfizer Limited (EP (GB) only), Pfizer Inc (EP except GB / US / JP)
OS Homo sapiens
FN JP 2003024082-A/1
PD 28-JAN-2003
PF 17-JAN-2002 JP 2002008881
PR 23-JAN-2001 GB 0101739.1
PI harland lee
CC
FH Key Location/Qualifiers.

FEATURES
source
1. .918
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 918; DB 6; Length 918;
Best Local Similarity 100.0%; Pred. No. 1.7e-225;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAACTCCAGGAATTCCTTTGGGATCCTATAGTGACACCCCACTTA 60
DB 1 ATGCTGGCCACAACTCCAGGAATTCCTTTGGGATCCTATAGTGACACCCCACTTA 60
QY 61 ATCAGCCTCACTCATAGTGTATTATGGCGGCTGTGGTGTCAATTCATCTTTTC 120
DB 61 ATCAGCCTCACTCATAGTGTATTATGGCGGCTGTGGTGTCAATTCATCTTTTC 120
QY 121 CTCTGGTGAATGAAACCCGGTCAGTACCACCATGCGGTCAATTAATCTGGTGG 180
DB 121 CTCTGGTGAATGAAACCCGGTCAGTACCACCATGCGGTCAATTAATCTGGTGG 180
QY 181 GTCCACAGCGTTTTCGTGACAGTCCCAATTCGTGTGACCTACCTATCAAGAGACT 240
DB 181 GTCCACAGCGTTTTCGTGACAGTCCCAATTCGTGTGACCTACCTATCAAGAGACT 240
QY 241 TGGATGTTGGCTGCCCTTCGCAATTTGTAGTGCCATGCTGCACATCCACATGTAC 300
DB 241 TGGATGTTGGCTGCCCTTCGCAATTTGTAGTGCCATGCTGCACATCCACATGTAC 300
QY 301 CTCACGTTCTATTATGTGGTGATCCTGGTACCAGATACCTCATCTTCTCAAGTGC 360
DB 301 CTCACGTTCTATTATGTGGTGATCCTGGTACCAGATACCTCATCTTCTCAAGTGC 360
QY 361 AAAGACAAAGTGAATTTACAGAAACTGCTGCTGCCAGTGTGGCATGTGG 420
DB 361 AAAGACAAAGTGAATTTACAGAAACTGCTGCTGCCAGTGTGGCATGTGG 420
QY 421 ACGTGTGTGATTGTCATTGTGGTACCCCTGCTGCTCCCGGTATGGAATCCATGAGAA 480
DB 421 ACGTGTGTGATTGTCATTGTGGTACCCCTGCTGCTCCCGGTATGGAATCCATGAGAA 480
QY 481 TACAATGAGGAGCACTGTTTAAATTTTCAAGAGCTTCTTACACATATGTGAATC 540
DB 481 TACAATGAGGAGCACTGTTTAAATTTTCAAGAGCTTCTTACACATATGTGAATC 540
QY 541 ATCAACTATATGATGATGATTTTGTATAGCCCTGCTGTGATTTCTGTGGTCTTCCAG 600
DB 541 ATCAACTATATGATGATTTTGTATAGCCCTGCTGTGATTTCTGTGGTCTTCCAG 600
QY 601 GTCTTCATCATATGTTGATGGTGAGAGTACGCCATCTTTTACTATCCACAGGAG 660
DB 601 GTCTTCATCATATGTTGATGGTGAGAGTACGCCATCTTTTACTATCCACAGGAG 660
QY 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTTCATCTTGTGTTCTTCTTCCC 720
DB 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTTCATCTTGTGTTCTTCTTCCC 720
QY 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGAGCAATTCATTCATGCTTAAACAGC 780
DB 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGAGCAATTCATTCATGCTTAAACAGC 780

QY 781 AAGTTTGCAATTTTAAACGAAATCTTCTTGAGTGTAAACAGCAATTAGCTCTATGATTG 840
DB 781 AAGTTTGCAATTTTAAACGAAATCTTCTTGAGTGTAAACAGCAATTAGCTCTATGATTG 840
QY 841 CTCTCTTTTGTCTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 900
DB 841 CTCTCTTTTGTCTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 900
QY 901 TGTGTTTGTGCTCTTAG 918
DB 901 TGTGTTTGTGCTCTTAG 918

RESULT 5
AY288420 918 bp mRNA linear PRI 08-DEC-2003
LOCUS Homo sapiens G protein-coupled receptor 141 (GPR141) mRNA, complete cds.
DEFINITION
ACCESSION AY288420
VERSION AY288420.1 GI:32165523
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 918)
AUTHORS Fredriksson, R., Hoglund, P.J., Gloriam, D.E., Lagerstrom, M.C. and Schioth, H.B.
TITLE Seven evolutionarily conserved human rhodopsin G protein-coupled receptors lacking close relatives
JOURNAL FEBS Lett. 554 (3), 381-388 (2003)
MEDLINE 22985413
PURVED 14623098
REFERENCE 2 (bases 1 to 918)
AUTHORS Fredriksson, R., Hoglund, P.J., Gloriam, D.B.I., Lagerstrom, M.C. and Schioth, H.B.
TITLE Direct Submission
JOURNAL Submitted (30-APR-2003) Neuroscience; Unit of Pharmacology, Uppsala University, Box 593, Uppsala 75124, Sweden
FEATURES
source
1. .918
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1. .918
/gene="GPR141"
1. .918
/gene="GPR141"
/codon_start=1
/product="G protein-coupled receptor 141"
/protein_id="AAP72129.1"
/db_xref="GI:32165524"
/translation="MPGHTSRNSSCDPIVTPHLISLYFVLIGLVGVISILFLVKNTRSVTMAVINLWVHSVELLTPRLTYLIKKTMFGLPFCKFVSAMLIHMYLTFLFVYVILTRVLIFFKCKDKVFRKHAASAGMTLVIVVPLVSRVGRYHIEEYNEHCDFEKLHAYTKIINMYVIFVIAVAVILLVFOVFIIMLVQKRLSHLSEQFMAQLKRLFFGVLVLCPLPYQFPRIYINLVNTHSNACKSKAFYNEIFLSVTAISCYDLLLFFVGGSHMPKQKIIGLWNCVLCR"

ORIGIN
Query Match 100.0%; Score 918; DB 9; Length 918;
Best Local Similarity 100.0%; Pred. No. 1.7e-225;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAACTCCAGGAATTCCTTTGGGATCCTATAGTGACACCCCACTTA 60
DB 1 ATGCTGGCCACAACTCCAGGAATTCCTTTGGGATCCTATAGTGACACCCCACTTA 60
QY 61 ATCAGCCTCACTCATAGTGTATTATGGCGGCTGTGGTGTCAATTCATCTTTTC 120
DB 61 ATCAGCCTCACTCATAGTGTATTATGGCGGCTGTGGTGTCAATTCATCTTTTC 120

Db	601	GTCTTCATCATATGTTGATGGTGCAGAAAGCTACGCCACTCTTTACTATATCCACAGGAG	660
Qy	661	TTCTGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTTGTGTTCTTCCCTCCC	720
Db	661	TTCTGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTTGTGTTCTTCCCTCCC	720
Qy	721	TACCAGTTCTTTAGGATCTATTACTGAAATGTTGTGACGATTCACCAATGCTGTAAAGC	780
Db	721	TACCAGTTCTTTAGGATCTATTACTGAAATGTTGTGACGATTCACCAATGCTGTAAAGC	780
Qy	781	AAGGTTGCATTTTAAAGCAATCTTCTTGAGTGAACAGCAATAGCTGCTATGATTG	840
Db	781	AAGGTTGCATTTTAAAGCAATCTTCTTGAGTGAACAGCAATAGCTGCTATGATTG	840
Qy	841	CTTCTCTTTGCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT	900
Db	841	CTTCTCTTTGCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT	900
Qy	901	TGTGTTTGTGCGGTTAG 918	
Db	901	TGTGTTTGTGCGGTTAG 918	
RESULT 3			
BD105324		918 bp DNA linear PAT 27-AUG-2002	
LOCUS		Novel G protein-coupled receptor protein and its DNA.	
DEFINITION		Novel G protein-coupled receptor protein and its DNA.	
ACCESSION		BD105324	
VERSION		BD105324.1 GI:22650898	
KEYWORDS		WO 0196567-A/1.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.	
TITLE		Moriya.T., Ito.T., Shintani.Y. and Miyajima.N.	
JOURNAL		Novel G protein-coupled receptor protein and its DNA	
COMMENT		Patent: WO 0196567-A 1 20-DEC-2001;	
		TAKEDA CHEMICAL INDUSTRIES LTD, TAKEO MORIYA, TAKASHI ITO, YASUSHI	
		SHINTANI, NOBUYUKI MIYAJIMA	
		OS Homo sapiens (human)	
		PN WO 0196567-A/1	
		PD 20-DEC-2001	
		PF 14-JUN-2001 WO 2001JP005061	
		PR 15-JUN-2000 JP 00P 184596.19-JUL-2000 JP 00P 223887 PI	
		TAKEO MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC	
		C12N15/12, C12N1/21, C07K14/705, C07K16/28, C12P21/02, C12Q1/68, PC	
		A61K38/00,	
		PC A61K45/00, A61K48/00, A61P1/00, A61P3/10, A61P9/00, A61P25/28, PC	
		A61P29/00,	
		PC A61P35/00, A61P37/00, G01N33/15, G01N33/50, G01N33/566//	
		PC (C12N1/21, C12R1:19), (C12P21/02, C12R1:19)	
		CC Novel G protein-coupled receptor protein and its DNA FH Key	
FT	source	Location/Qualifiers	
FT	1. 918	/organism='Homo sapiens (human)'	
FEATURES		Location/Qualifiers	
source	1. 918	/organism='Homo sapiens'	
		/mol_type='genomic DNA'	
		/db_xref='taxon:9606'	
ORIGIN			
Query Match		100.0%; Score 918; DB 6; Length 918;	
Best Local Similarity		100.0%; Pred. No. 1.7e-225;	
Matches 918; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGCGTGGCCAAATACCTCCAGGATTCCTCTTGGATCCCTATAGTGACACCCACATTA	60
Db	1	ATGCGTGGCCAAATACCTCCAGGATTCCTCTTGGATCCCTATAGTGACACCCACATTA	60
Qy	61	ATCAGCCTCTACTTCATAGTGTATTATGGCGGGCTGGTGGTGCATTTCCATTTCTTTTC	120

Db	61	ATCAGCCTCTACTTCATAGTGTATTATGGCGGGCTGGTGGTGCATTTCCATTTCTTTTC	120
Qy	121	CTCTGGTGAATAATGAACACCCGGTCACTGACCAACATGGCGGTCAATTAATCTGGTGTG	180
Db	121	CTCTGGTGAATAATGAACACCCGGTCACTGACCAACATGGCGGTCAATTAATCTGGTGTG	180
Qy	181	GTCCACAGGTTTCTGCTGACAGTGCATTTGCTTGGCTTACCTCTCATCAAGAAGACT	240
Db	181	GTCCACAGGTTTCTGCTGACAGTGCATTTGCTTGGCTTACCTCTCATCAAGAAGACT	240
Qy	241	TGATCTTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGGCATCTGTCACATCCACATGTAC	300
Db	241	TGATCTTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGGCATCTGTCACATCCACATGTAC	300
Qy	301	CTCAGTTCTCTATTCTATGTGCTGATCTGCTGACAGATACCTCATCTTCTTCAAGTGC	360
Db	301	CTCAGTTCTCTATTCTATGTGCTGATCTGCTGACAGATACCTCATCTTCTTCAAGTGC	360
Qy	361	AAAGACAAAAGTGGAAATCTACAGAAAACCTGCATGCTGGCTGCCAGTCTGGCATGTGG	420
Db	361	AAAGACAAAAGTGGAAATCTACAGAAAACCTGCATGCTGGCTGCCAGTCTGGCATGTGG	420
Qy	421	ACGCTGGTGAATGTCATTTGTTGTAACCTTCCCTGGTGTCTCCGGTATGGATCCATGAGAA	480
Db	421	ACGCTGGTGAATGTCATTTGTTGTAACCTTCCCTGGTGTCTCCGGTATGGATCCATGAGAA	480
Qy	481	TACAAATGAGGACACATGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC	540
Db	481	TACAAATGAGGACACATGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC	540
Qy	541	ATCAATATATGATGATCAATTTTGTGCATAGCGGTTGCTGTGATTTCTGTGTTCTTCCAG	600
Db	541	ATCAATATATGATGATCAATTTTGTGCATAGCGGTTGCTGTGATTTCTGTGTTCTTCCAG	600
Qy	601	GTCTTCATCATATGATGTTGATGTTGAGTGCAGAGTACGCACTCTTACTATCCACACAGGAG	660
Db	601	GTCTTCATCATATGATGTTGATGTTGAGTGCAGAGTACGCACTCTTACTATCCACACAGGAG	660
Qy	661	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCTTCCC	720
Db	661	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCTTCCC	720
Qy	721	TACAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTGTAAACAGC	780
Db	721	TACAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTGTAAACAGC	780
Qy	781	AAGTTGCATTTTATACCGAAATCTTCTTGAGTGAACAGCAATTTAGCTGTATGATTG	840
Db	781	AAGTTGCATTTTATACCGAAATCTTCTTGAGTGAACAGCAATTTAGCTGTATGATTG	840
Qy	841	CTTCTCTTTGCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT	900
Db	841	CTTCTCTTTGCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATTAATGGCTTATGGAAT	900
Qy	901	TGTGTTTGTGCGGTTAG 918	
Db	901	TGTGTTTGTGCGGTTAG 918	
RESULT 4			
BD187510		918 bp DNA linear PAT 17-JUL-2003	
LOCUS		Novel Polypeptide.	
DEFINITION		Novel Polypeptide.	
ACCESSION		BD187510	
VERSION		BD187510.1 GI:32997249	
KEYWORDS		JP 2003024082-A/1.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.	
		1 (bases 1 to 918)	
		Lee,H.	

Pfizer Limited (GB) ; PFIZER INC. (US)
Location/Qualifiers
1. .918
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 100.0%; Score 918; DB 6; Length 918;
Best Local Similarity 100.0%; Pred. No. 1.7e-225; Indels 0; Gaps 0;
Matches 918; Conservative 0; Mismatches 0;

1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCCTATAGTGACACCCCACTTA 60
1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCCTATAGTGACACCCCACTTA 60
61 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGTGTCTATTCATTCCTTTTC 120
61 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGTGTCTATTCATTCCTTTTC 120
121 CTCCTGGTGAATAATGAACACCCGGTCAGTGACACCAATGGCGGTCAATTAACCTTGGTGGT 180
121 CTCCTGGTGAATAATGAACACCCGGTCAGTGACACCAATGGCGGTCAATTAACCTTGGTGGT 180
181 GTCCACAGCGTTTCTGTGTGACAGTGCATTTGCGCTTGACCTACTCATCAAGAAGACT 240
181 GTCCACAGCGTTTCTGTGTGACAGTGCATTTGCGCTTGACCTACTCATCAAGAAGACT 240
241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATCTGCACATCCACATGTAC 300
241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATCTGCACATCCACATGTAC 300
301 CTCAGCTTCTATCTATGTGTGATCCCTGGTTCACAGATACCTCATCTTCTCAAGTGC 360
301 CTCAGCTTCTATCTATGTGTGATCCCTGGTTCACAGATACCTCATCTTCTCAAGTGC 360
361 AAGACAAAGTGGAAATTTACAGAAAATTCAGTGGCTGGTGGTGTCTATTCATTCCTTTTC 420
361 AAGACAAAGTGGAAATTTACAGAAAATTCAGTGGCTGGTGGTGTCTATTCATTCCTTTTC 420
421 ACGCTGGTGAATGTCTATGTGTGATCCCTGGTTCACAGATACCTCATCTTCTCAAGTGC 480
421 ACGCTGGTGAATGTCTATGTGTGATCCCTGGTTCACAGATACCTCATCTTCTCAAGTGC 480
481 TACAATGAGGAGCAGCTGTTTTTAAATTTACAAAAGAGCTTGTCTTACACATATGTGAAAATC 540
481 TACAATGAGGAGCAGCTGTTTTTAAATTTACAAAAGAGCTTGTCTTACACATATGTGAAAATC 540
541 ATCAACTATATGATAGTCAATTTTGTGATAGCGGTTCCTGCTGATTCCTGTTGGTCTTCCAG 600
541 ATCAACTATATGATAGTCAATTTTGTGATAGCGGTTCCTGCTGATTCCTGTTGGTCTTCCAG 600
901 TGTGTTTGTGCGGCTTAG 918

Db 901 TGTGTTTGTGCGGCTTAG 918

RESULT 2
AX498180
LOCUS
DEFINITION Sequence 3 from Patent WO0242461.
ACCESSION AX498180
VERSION AX498180.1 GI:23343111
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chen, R., Chu, Z. L., Dang, H. T., Lowitz, K. P. and Pride, C.
TITLE Endogenous and non-endogenous versions of human g protein-coupled receptors
JOURNAL Patent: WO 0242461-A 3 30-MAY-2002;
Arena Pharmaceuticals, Inc. (US)
FEATURES
source 1. .918
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 918;
Best Local Similarity 100.0%; Pred. No. 1.7e-225; Indels 0; Gaps 0;
Matches 918; Conservative 0; Mismatches 0;

Qy 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCCTATAGTGACACCCCACTTA 60
Db 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCCTATAGTGACACCCCACTTA 60
Qy 61 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGTGTCTATTCATTCCTTTTC 120
Db 61 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGTGTCTATTCATTCCTTTTC 120
Qy 121 CTCCTGGTGAATAATGAACACCCGGTCAGTGACACCAATGGCGGTCAATTAACCTTGGTGGT 180
Db 121 CTCCTGGTGAATAATGAACACCCGGTCAGTGACACCAATGGCGGTCAATTAACCTTGGTGGT 180
Qy 181 GTCCACAGCGTTTCTGTGTGACAGTGCATTTGCGCTTGACCTACTCATCAAGAAGACT 240
Db 181 GTCCACAGCGTTTCTGTGTGACAGTGCATTTGCGCTTGACCTACTCATCAAGAAGACT 240
Qy 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATCTGCACATCCACATGTAC 300
Db 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATCTGCACATCCACATGTAC 300
Qy 301 CTCAGCTTCTATCTATGTGTGATCCCTGGTTCACAGATACCTCATCTTCTCAAGTGC 360
Db 301 CTCAGCTTCTATCTATGTGTGATCCCTGGTTCACAGATACCTCATCTTCTCAAGTGC 360
Qy 361 AAGACAAAGTGGAAATTTACAGAAAATTCAGTGGCTGGTGGTGTCTATTCATTCCTTTTC 420
Db 361 AAGACAAAGTGGAAATTTACAGAAAATTCAGTGGCTGGTGGTGTCTATTCATTCCTTTTC 420
Qy 421 ACGCTGGTGAATGTCTATGTGTGATCCCTGGTTCACAGATACCTCATCTTCTCAAGTGC 480
Db 421 ACGCTGGTGAATGTCTATGTGTGATCCCTGGTTCACAGATACCTCATCTTCTCAAGTGC 480
Qy 481 TACAATGAGGAGCAGCTGTTTTTAAATTTACAAAAGAGCTTGTCTTACACATATGTGAAAATC 540
Db 481 TACAATGAGGAGCAGCTGTTTTTAAATTTACAAAAGAGCTTGTCTTACACATATGTGAAAATC 540
Qy 541 ATCAACTATATGATAGTCAATTTTGTGATAGCGGTTCCTGCTGATTCCTGTTGGTCTTCCAG 600
Db 541 ATCAACTATATGATAGTCAATTTTGTGATAGCGGTTCCTGCTGATTCCTGTTGGTCTTCCAG 600
Qy 601 GTCTTCATCATTTATGTTGATGGTGCAGAGCTACGCCACTCTTCTTACTATCCACCAGGAG 660

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 25, 2004, 12:45:39 ; Search time 3929 Seconds
(without alignments)
10126.980 Million cell updates/sec
Title: US-10-055-106C-1
Perfect score: 918
Sequence: 1 atgcctggccacaataacctc.....attgtgtttgtgcgcttag 918

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pi.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_on.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pi.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rdi.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	918	100.0	918	6	AX481576	AX481576 Sequence
2	918	100.0	918	6	AX498180	AX498180 Sequence
3	918	100.0	918	6	BD105324	BD105324 Novel G p
4	918	100.0	918	6	BD187510	BD187510 Novel Pol
5	918	100.0	918	9	AY288420	AY288420 Homo sapi
6	918	100.0	1336	6	AX709193	AX709193 Sequence
7	918	100.0	1340	6	AX709194	AX709194 Sequence
8	918	100.0	1460	6	AX709195	AX709195 Sequence
9	918	100.0	2525	6	AX147836	AX147836 Sequence
10	918	100.0	2525	6	AX521885	AX521885 Sequence
11	918	100.0	113306	6	AX646815	AX646815 Sequence
12	918	100.0	218186	9	AC083865	AC083865 Homo sapi
13	916.4	99.8	1051	6	AX453412	AX453412 Sequence
14	913.2	99.5	164055	2	AC146385	AC146385 Pan trogl
15	895	97.5	1499	6	AX451925	AX451925 Sequence
16	690	75.2	972	6	AX657538	AX657538 Sequence
17	636.4	69.3	918	10	AY288427	AY288427 Mus muscu
18	636.4	69.3	206999	10	AC122886	AC122886 Mus muscu
19	634.8	69.2	167316	2	AC078995	AC078995 Mus muscu
20	525	57.2	228766	2	AC099132	AC099132 Rattus no
21	455	49.7	456	9	AY255538	AY255538 Homo sapi
22	437.2	47.6	140539	2	AC079758	AC079758 Homo sapi
23	433	47.2	744	10	AY288432	AY288432 Rattus no
24	390	42.5	447	6	AX147776	AX147776 Sequence
25	390	42.5	447	6	AX521825	AX521825 Sequence
26	276.8	30.2	393	10	AY255553	AY255553 Mus muscu
27	184	20.0	169095	5	BX088685	BX088685 Zebrafish
28	184	20.0	188535	2	BX640482	BX640482 Danio rer
29	144.8	15.8	897	6	BD182016	BD182016 Novel G p
30	105	11.4	140539	2	AC079758	AC079758 Homo sapi
31	105	11.4	225912	2	AC084210	AC084210 Homo sapi
32	76.4	8.3	1113	6	AX280917	AX280917 Sequence
33	76.4	8.3	1113	9	AY268428	AY268428 Homo sapi
34	76.4	8.3	1252	9	HUMOPRLP	L40949 Homo sapien
35	76.4	8.3	1379	9	AF348323	AF348323 Homo sapi
36	76.4	8.3	1805	6	AX746239	AX746239 Sequence
37	76.4	8.3	1973	6	AR270828	AR270828 Sequence
38	76.4	8.3	1973	6	AR380872	AR380872 Sequence
39	76.4	8.3	1973	9	HSORL1	X77130 H.sapiens m
40	76.4	8.3	2534	6	AX548923	AX548923 Sequence
41	76.4	8.3	2534	9	HSU30185	U30185 Human orpha
42	76.4	8.3	3420	9	BC038433	BC038433 Homo sapi
43	73.2	8.0	1134	6	AR404125	AR404125 Sequence
44	73.2	8.0	1134	9	AF126470	AF126470 Homo sapi
45	73.2	8.0	239344	2	AC133310	AC133310 Rattus no

ALIGNMENTS

RESULT 1
AX481576
LOCUS AX481576 918 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 1 from Patent Ep1225183.
ACCESSION AX481576
VERSION AX481576.1 GI:22316490
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Harland, L.
TITLE Human g-protein coupled receptor
JOURNAL Patent: EP 1225183-A 1 24-JUL-2002;

```
QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db |||||
381 ATGCTTGGCCACCAATACCTCCAGAAATCTCTTGGATCCTATAGTGACACCCACCTTA 440
QY 21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db |||||
441 ATCAGGCTCTACTTCATAGTGTCTATTGGGGGCTGGTGGGTGTCAATTCATCTTTC 500
QY 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
Db |||||
501 CTCCTGGTGAATAATGAACACCCCGTCAGTGACCAATGGCGTCAATTAACCTGGTGGTG 560
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
Db |||||
561 GTCCACAGAGGTTTCTGTGTGACAGTGCCATTTCGCTTGACCTCATCAGAGAGCT 620
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db |||||
621 TGGATGTTTGGGCTGGCCCTCTGCAAAATTTGTAGTGCCATGCTGCCATGCCATGTAC 680
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db |||||
681 CTCACGTTTCTATTCTATGTGGTGATCCTGGTCACCAATACCTCATCTCTCTCAAGTC 740
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLysAlaGlyMetTrp 140
Db |||||
741 AAAGACAAAGTGGAAATCTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCCATGTGG 800
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db |||||
801 AGCTGGTGATGTGATGTGGTACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAA 860
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
Db |||||
861 TACAATGAGGAGCACCTGTTTAAATTTCAAAAGAGCTTGTCTACACATATGTGAAATC 920
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
Db |||||
921 ATCAACTATATGATAGTCAATTTTGTGATAGCCGTTGCTGTGATTCTGTGTCTTCCAG 980
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db |||||
981 GTCTTCATCATTTATGTTGATGTGTGCAGAGCTACGCCACTCTTTACTATCCCAAGGAG 1040
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db |||||
1041 TTCTGGGCTCAGCTGAAACCACTAATTTTATAGGGGTCTATCCTGTTGTTTCTCTTCC 1100
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260
Db |||||
1101 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGATTCCTATGCCCTGTACAGC 1160
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db |||||
1161 AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAAACCAATTAGCTGTCTATGATTG 1220
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
Db |||||
1221 CTTCTCTTTGCTTTGGGGAGCCATTTGTTTACGAAAGATAT-TGGCTATGGAAAT 1279
QY 301 CysValLeuCysArg 305
Db |||||
1280 TGTGT-TTGTGCCGT 1293
```

Search completed: April 25, 2004, 20:14:16
Job time : 469 secs

US-10-055-106C-2 (1-305) x AAL53413 (1-1684)

Qy 1 MetProGlyHisAsnThrSerArgHisSerCysAspProlleValThrProHisLeu 20
Db 171 ATGCTGGCCCAATACCTCCAGGAATTCCTCTTGGATCCTATAGTACACCCACCTTA 230
Qy 21 IleSerLeuTyrPheIleValLeuLeuGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db 231 ATCAGCCCTCTACTTCATAGTGTCTATTGGCGGCTGGTGGGTGATCATTTCCATCTCTTC 290
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
Db 291 CTCCTGGTGAATAATGAACACCGGTCAGTGACCAACATGGGGTCATTAACCTTGGTGTG 350
Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysIleValThr 80
Db 351 GTCCACACGCGTTTCTCTGACAGTGCCATTTGCTTGACCTACCTCATCAAGAAGACT 410
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 411 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCATGTAC 470
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db 471 CTCACGTTCTTATCTATGTGTGATCTCTGTCCACAGATACCTCATCTTCTTCAAGTGC 530
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrp 140
Db 531 AAGACAAAGTGGAAATCTACAGAAATCGCATGCTGTGGCTGCCAGTGTGGCATGTGG 590
Qy 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 591 ACGCTGGTGATTGTTCATTTGTGTGATGCTGTGTCCTCCGTTATGGAATCCATGAGAA 650
Qy 161 TyrSerGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
Db 651 TACATAGAGAGCACTGTTTAAATTCACAAAGAGCTTGCTTACACATATGTGAATC 710
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 711 ATCAACTATATGATAGTCATTTTGTGTGATGCTGTGATGCTGTGTTGTTGTTCCAG 770
Qy 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGluGlu 220
Db 771 GTCTTCATCATATGTTGATGGTGAGAGCTAGCCACTCTTTTACTATCCACAGGAG 830
Qy 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 831 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTCTATCTTGTGTTCTTCTTCCC 890
Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 891 TACCAGTTCTTTAGGATCTATCTACTTGAATTTGTGAGCGCATTCATGCTGTAGCAGC 950
Qy 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 951 AAGTTGCAATTTTATACGAATCTTCTTGTAGTGTACAGCAATAGCTGCTATGATTG 1010
Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
Db 1011 CTTCTCTTTGTCTTTGGGGGAAGCCATTTGGTTTAAGCAAAAGATAATTTGGCTTATGAAT 1070
Qy 301 CysValLeuCysArg 305
Db 1071 TGTGTTTGTGCCGT 1085

RESULT 15

AAD37670

ID AAD37670 standard; cDNA; 1499 BP.

XX

AC AAD37670;

XX

DT 27-AUG-2002 (first entry)

XX Human G-protein coupled receptor-6 (GCRC-6) cDNA.

XX Human; G-protein coupled receptor-6; GCRC-6; atherosclerosis; cancer;
cell proliferative disorder; gastrointestinal; autoimmune; metabolic;
neurological; inflammatory; cardiovascular; viral infection; anorexia;
cirrhosis; multiple sclerosis; Huntington's disease; gene therapy;
Alzheimer's disease; heart failure; hepatitis; cholecystitis; obesity;
rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris;
osteoporosis; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 381..1400

XX /tag= a

XX /product= "Human GCRC-6 protein"

XX WO200226825-A2.

XX 04-APR-2002.

XX 28-SEP-2001; 2001WO-US030661.

XX 29-SEP-2000; 2000US-0236546P.

XX 13-OCT-2000; 2000US-0240589P.

XX 20-OCT-2000; 2000US-0242232P.

XX 20-OCT-2000; 2000US-0242322P.

XX 03-NOV-2000; 2000US-0245855P.

XX 03-NOV-2000; 2000US-0245900P.

XX 15-NOV-2000; 2000US-0247587P.

XX 15-NOV-2000; 2000US-0249343P.

XX (INCY-) INCYTE GENOMICS INC.

XX Baughn ME, Graul RC, Walia NK, Gandhi AR, Hafalia AJA;

XX Ramkumar J, Tribouley CM, Thornton M, Kallick DA, Yao MG;

XX Elliott VS, Burford N, Khan FA, Yue H, Lu Y, Arvizu C, Roopa R;

XX Nguyen DB, Lee EA, Lu DAM, Ison CH, Walsh RT, Policky JL;

XX WPI; 2002-426012/45.

XX P-PSDB; AAE23414.

XX Novel G-protein coupled receptor polypeptides referred as GCRC peptides,

XX useful for treating multiple sclerosis, cholecystitis heart failure,

XX angina pectoris, rheumatoid arthritis, obesity, osteoporosis.

XX Claim 83; Page 140; 147pp; English.

XX The invention relates to human G-protein coupled receptor (GCRC 1-16)

XX polypeptides and polynucleotides. Sequences of the invention are useful

XX for the diagnosis, treatment and prevention of cell proliferative (e.g.

XX cancer, cirrhosis), neurological (e.g. multiple sclerosis, Huntington's

XX disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris,

XX heart failure), gastrointestinal (e.g. anorexia, cholecystitis),

XX autoimmune/inflammatory (rheumatoid arthritis, Hashimoto's thyroiditis)

XX and metabolic disorders (e.g. obesity, osteoporosis), viral infections,

XX atherosclerosis and hepatitis. GCRC proteins are useful for identifying

XX compounds that modulate, mimic and block olfactory and taste sensations.

XX They are also useful for identifying GCRC modulators. GCRC DNAs are

XX useful in gene therapy. The present sequence is human GCRC-6 cDNA

XX SQ Sequence 1499 BP; 375 A; 340 C; 329 G; 455 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 1,03e-124 Length: 1499

XX Score: 1547.00 Matches: 303

XX Percent Similarity: 99.34% Conservative: 0

XX Best Local Similarity: 99.34% Mismatches: 2

XX Query Match: 97.17% Indels: 2

XX DB: 6 Gaps: 0

XX US-10-055-106C-2 (1-305) x AAD37670 (1-1499)

Db 12080 ATCAACTATATGATGTCATTTTGTATAGCGGTGCTGATTCCTGCTTCACG 12139
 Qy 201 ValPheIleIleMetLeuMetValGlnLeuLeuArgHisSerLeuLeuSerHisGlnGlu 220
 Db 12140 GTCCTTCATCATATGTTGATGGTGAGAGCTAGCCCACTCTTTTACATATCCACGAG 12199
 Qy 221 PheTrpAlaGlnLeuLeuAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
 Db 12200 TTCGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTGTTGTTGTTCTTCCC 12259
 Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
 Db 12260 TACCAGTTCCTTAGCATCTATTACTTGAATGTTGACGCAATCCCAATGCCCTGTAACAGC 12319
 Qy 261 LysValAlaPheTyrAsnGlnIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
 Db 12320 AAGGTTGATTTTATACGAATCTCTTGAGTGACAGCAATAGCTGCTATGATTTG 12379
 Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLeuGlnIleValIleGlyLeuTrpAsn 300
 Db 12380 CTTCCTCTTGCTTTGGGGGAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 12439
 Qy 301 CysValLeuCysArg 305
 Db 12440 TGTGTTTGTGCCGT 12454
 RESULT 13
 AAL53414
 ID AAL53414 standard; DNA; 939 BP.
 AC AAL53414;
 XX
 DT 12-DEC-2002 (first entry)
 DE 939 nt coding DNA of a human G-protein coupled receptor type protein.
 KW Anti-HIV; cytostatic; antidiabetic; antiasthmatic; antiinflammatory;
 KW haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;
 KW antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;
 KW cardiac; dermatological; antinfertility; hepatotropic; antiallergic;
 KW antipsoriatic; ophthalmological; antianigmal; antithyroid; anticonvulsant;
 KW antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;
 KW 93870 receptor; immune; inflammatory disorder; platelet disorder;
 KW skeletal; bone metabolism disorder; bone marrow mononuclear disorder;
 KW cellular proliferative; differentiative disorder; hormonal disorder;
 KW neurological disorder; cardiovascular disorder; viral disease; pain;
 KW liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;
 KW hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;
 KW viral meningitis; fungal meningoencephalitis; multiple sclerosis;
 KW Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;
 KW Huntington's disease; heart failure; angina pectoris; dermatitis;
 KW myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;
 KW inflammatory bowel disease; asthma; graft-versus-host disease; allergy;
 KW conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;
 KW transgenic animal; human; gene; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 CDS 1..939
 FT /*tag= a
 FT /partial
 FT /product= "Human G-protein coupled receptor type protein
 FT 93870"
 FT /note= "No stop codon"
 XX
 PN WO200270657-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 28-FEB-2002; 2002WO-US006455.
 XX

PR 01-MAR-2001; 2001US-0272677P.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Glucksmann MA;
 DR WPI; 2002-732793/79.
 XX P-PSDB; AAO22919.
 XX
 PT New G-protein coupled receptor used in receptor assays as a target for
 PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and
 PT inflammatory disorders, platelet disorders, skeletal or bone metabolism
 PT disorders.
 XX
 PS Claim 5; Page 101-103; 105pp; English.
 XX
 CC The invention relates to an isolated polypeptide, which is a G-protein
 CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled
 CC receptor type proteins (GPCRs), designated the 93870 receptor. The
 CC polypeptides, nucleic acid molecules and antibodies of the invention are
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
 CC monitoring clinical trials or pharmacogenetics), or in methods of
 CC treatment (e.g. therapeutic and prophylactic). They are useful in
 CC treating and diagnosing conditions related to aberrant activity or
 CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and
 CC inflammatory disorders, platelet disorders, skeletal or bone metabolism
 CC disorders, or bone marrow mononuclear disorders, as well as cellular
 CC proliferative and/or differentiative disorders, hormonal disorders,
 CC neurological disorders, cardiovascular disorders, viral diseases, liver
 CC disorders, and pain and metabolic disorders. Conditions that can be
 CC treated include cancer, diabetes mellitus, hypothyroidism,
 CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or
 CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,
 CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,
 CC Huntington's disease, heart failure, angina pectoris, myocardial
 CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,
 CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host
 CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The
 CC transgenic animals are useful for studying the function and/or activity
 CC of a 93870 protein and for identifying and/or evaluating modulators of
 CC 93870 activities. The polynucleotides of the invention can be used in
 CC gene therapy. This polynucleotide sequence represents the 939 nucleotide
 CC DNA of the human G-protein coupled receptor type protein of the invention
 XX
 SQ Sequence 939 BP; 215 A; 212 C; 205 G; 307 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,09e-128 Length: 939
 Score: 1587.00 Matches: 304
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.67% Mismatches: 0
 Query Match: 99.69% Indels: 0
 DB: 6 Gaps: 0
 US-10-055-106C-2 (1-305) x AAL53414 (1-939)
 Qy 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
 Db 25 ATGCTGGCCACATATACCTCCAGGAATTCCTTGGATCCTATAGTACACCCCACTTA 84
 Qy 21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerLeuPhe 40
 Db 85 ATCAGCCTCTACTTCATATAGTGTCTTATTTGGCGGCTGTGGGTGTCATTTCCTTTTC 144
 Qy 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
 Db 145 CTCCTGGTGAATGAACACCCGGTCAGTGACCACCATCGCGGTCAATTAACCTGGTGGTG 204
 Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
 Db 205 GTCCACAGCGGTTTTCTCTGCTGACGTGCCATTTCGCTTGACCTACCTCATCAAGAGACT 264
 Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100


```
Db 207 GTCCACAGGTTTCTTCGTCGACAGTGCCATTCGCTGACCTACCTCATCAAGAAGACT 266
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 267 TGGATGTTTGGGCTGCGCTTCTGCAAAATTTGGAGTGCCATGCTGCATCCACATGATGAC 326
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db 327 CTCAGGTTCTTATCTATGTTGATGCTCTGGTCCACAGATACCTCATCTTCTCAAGTGC 386
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisIleValAlaValAlaSerAlaGlyMetTyr 140
Db 387 AAAGCAAAAGTGAATTTACAGAAACTGCATGCTGGCTGCCAGTGCCTGGCATGTGG 446
Qy 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 447 AGCTGGTGAATTTGATGTTGATGCTACCCCTGGTGTCTCCGGTATGGAATCCATCAGGAA 506
Qy 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
Db 507 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 566
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
Db 567 ATCAACTATATATAGTCAATTTTGTATAGCGCTTGTGATCTGTGCTCTTCCAG 626
Qy 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 627 GTCTTCATCATATGTTGATGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACCAGGAG 686
Qy 221 PheTyrAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 687 TTCTGGGCTCAGCTGAAACCTATTATTTATAGGGGTCTATCTGTTGTTCTTCTTCC 746
Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 747 TACCAGTCTTATAGATCTATTACTTATGATGTTGACGCAATTCCAATGCCGTGAACAGC 806
Qy 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 807 AAGGTTGCATTTTATACGAAATCTTCTTGAGGTAAACAGCAATTAGCTGCTATGATTG 866
Qy 281 LeuLeuPheValPheGlyGlySerHisTyrPheLysGlnLysIleIleGlyLeuTyrAsn 300
Db 867 CTTCCTTTGCTTTGGGGAAGCCATTGGTTTAACCAAAAGATAATTGGCTTATGGAAT 926
Qy 301 CysValLeuCysArg 305
Db 927 TGTGTTTGTGCGGT 941

RESULT 12
ADC86554 standard; DNA; 113306 BP.
XX
AC ADC86554;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR gene SEQ ID NO:1007.
XX
KW ds; gene; human; GPCR;
XX guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX
OS Homo sapiens.
XX
PN BP1270724-A2.
XX
XX 02-JAN-2003.
XX
XX 18-JUN-2002; 2002EP-00013517.
XX
XX 18-JUN-2001; 2001JP-00246789.
```

```
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX WPI; 2003-315783/31.
XX DR P-PSDB; ADC86555.
XX
XX New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 1; SEQ ID NO 1007; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC guanosine triphosphate-binding protein coupled receptor.
CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
CC invention.
XX
XX Sequence 113306 BP; 34476 A; 21483 C; 21391 G; 35956 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.67e-126 Length: 113306
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-055-106C-2 (1-305) x ADC86554 (1-113306)
Qy 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 11540 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTTGGCATCCTATAGTGACACCCACCTTA 11599
Qy 21 IleSerLeuTyrPheIleValIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 11600 ATCAGCTCTTACTTCAATAGTCTTATTTGGGGGCTGGTGGGTGTCATTTCCATTCCTTTC 11659
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
Db 11660 CTCCTGGTGAATGAACACCCGCTCAGTCACACCATCGCGGTCACTTAACCTGGTGGTG 11719
Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrIleuIleLysLysThr 80
Db 11720 GTCCACAGCGTTTTTCTGCTGACAGTGCCATTTGCTTGACCTACCTCATCAAGAAGACT 11779
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 11780 TGGATGTTTGGGCTGCGCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGATC 11839
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleuIlePhePheLysCys 120
Db 11840 CTCAGTTCCTATTTCTATGTTGGTATCTCTGTCACCAAGATACCTCATCTTCTTCAAGTGC 11899
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisIleValAlaValAlaSerAlaGlyMetTyr 140
Db 11900 AAAGCAAAAGTGAATTTCTACAGAAACTGCATGCTGTGCTGCCATGCTGGCATGTGG 11959
Qy 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 11960 ACGCTGGTGAATTTGATGTTGATGCTACCCCTGGTGTCTCCGGTATGGAATCCATCAGGAA 12019
Qy 161 TyrAsnGluGluHisCysPhePheHisLysGluLeuAlaTyrThrTyrValLysIle 180
Db 12020 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTCTTACATATGTGAAAATC 12079
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
```


Db 463 TCGATGTTGGGCTGCCCTCTGCAAAATTTGTGAGTGCCATGTCACATCATGATGAC 522
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLeuValCys 120
Db 523 CTCAGTTCCTATCTATGTTGGTATCTCTGTCACCATACCTCTCTTCAATGTC 582
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLalaSerAlaGlyMetTyr 140
Db 583 AAGACAAAGTGAATCTACAGAAAGTGCATGCTGTGGCTGCCAGTGTGGCATGTGG 642
Qy 141 ThrLeuValIleValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 643 ACGCTGGGATGTGATGTGATGTCCTGCTGCTCCCGTATGAATCCATGAGAA 702
Qy 161 TyrAsnGluGluHisCysPhePheHisLysGluLeuAlaTyrThrTyrValIle 180
Db 703 TACAATGAGGACGCTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC 762
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 763 ATCAACTATATGATAGTCATTTTGTGTCATAGCCGTGCTGTGATCTGTTGGTCTTCAG 822
Qy 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 823 GTCTTCATCATATGTTGATGTCAGAGAGCTAGCCACTCTTTACTATCCACAGAG 882
Qy 221 PheTrpAlaGlnLeuLysLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 883 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTCATCTGTTGTTTCTTCC 942
Qy 241 TyrGlnPhePheAspGlyTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 943 TACAGTCTTTAGATCTATCTTGTATGTTGTGAGCATTCATGCTGTAAAGC 1002
Qy 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 1003 AAGGTTGCATTTTATACGAAATCTCTTGAGTGTAAAGCAATAGCTGATGATTG 1062
Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
Db 1063 CTTCCTTTGCTTTGGGGAGGACCATGTTGTTTAAAGCAAGATTAATGGCTTATGAAT 1122
Qy 301 CysValLeuCysArg 305
Db 1123 TGTGTTTGTGCGGT 1137
RESULT 9
AAF88585
ID AAF88585 standard; cDNA; 1460 BP.
AC AAF88585;
XX 19-NOV-2002 (first entry)
DT Human GCRC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54.
XX
DE GCRC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
KW cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
KW cerebrotrophic; antinflammatory; virucide; antibacterial; fungicide;
KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
KW Parkinson's disease; Crohn's disease; constipation; infection;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200263004-A2.
XX
XX 15-AUG-2002.
XX
XX 06-FEB-2002; 2002WO-US003635.
XX
XX 07-FEB-2001; 2001US-0267322P.
XX

PR 23-FEB-2001; 2001US-0271215P.
PR 08-MAR-2001; 2001US-0274551P.
PR 23-MAR-2001; 2001US-0278507P.
PR 30-MAR-2001; 2001US-0280597P.
PR 02-APR-2001; 2001US-0281107P.
PR 06-APR-2001; 2001US-0282121P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX Baughn WR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;
PI Kallick DA, Gandhi AR, Wallia NK, Arvizu C, Elliott VS, Hafalia AJA;
PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
PI Warren BA, Yang J, Lee EA, Harland L;
XX
XX WPI; 2002-627557/67.
DR P-PSDB; AAB71327.
XX
XX New human G-protein coupled receptors (GCRC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT over expression of functional GCRCs e.g. cancer, Alzheimer's and
PT Parkinson's.
XX
XX Claim 115; Page 213-214; 239pp; English.
XX
XX This invention describes novel polypeptides which have anti-HIV,
CC antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,
CC hepatotropic, laxative, cerebrotrophic, antinflammatory, virucide,
CC antibacterial, fungicide and protozoacide activity. The products of the
CC invention are useful for treating a disease or condition associated with
CC decreased expression or over expression of functional G-protein coupled
CC receptors (GCRC), while antibodies generated against the polypeptide of
CC the invention are useful for diagnosing a condition or disease associated
CC with the expression of GCRC e.g. arteriosclerosis, cirrhosis, cancer,
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
CC The compounds described in the invention can be used for gene therapy.
CC AAF88580-AAF88627 encode the GCRC proteins represented by AAB71322-
CC AAB71369, described in the disclosure of the invention
XX
XX Sequence 1460 BP; 363 A; 327 C; 316 G; 454 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.27e-128 Length: 1460
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-055-106c-2 (1-305) x AAF88585 (1-1460)
Qy 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
Db 343 ATGCTGGCCACAAATACCTCCAGGAATTCCTTTGGATCCTATAGTACACCCACTTA 402
Qy 21 IleSerLeuTyrPheIleValIleGlyLeuValGlyValIleSerLeuPhe 40
Db 403 ATCAGCCTCTACTTCATAGTCTTATTTGGGGCTGGTGGTGCATTTCCATTTCTTTTC 462
Qy 41 LeuLeuValIysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 463 CTCCTGGTGAATGAATGACACCCGGTCAGTACACCATCGCGTCATTAACTTGGTGGTG 522
Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysThr 80
Db 523 GTCCACAGGGTTTTCTGCTGACAGTCCCATTTGCTTGACCTACCTCATCAAGAAGACT 582
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisMetTyr 100
Db 583 TGGATGTTTGGGCTGCCCTCTGCAAAATTTGAGTGGCCATGCTGCACATCCATGTAC 642
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120

```
DB 399 GTCCACAGCGTTTCTGCTGACAGTGCCTTTCGCTTACCTACCTCATCAAGAGACT 458
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
DB 459 TGGATGTTGGGCTGCGCTTCTCAAAATTTGTGAGTGCCATGTCACATCCACATGTAC 518
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
DB 519 CTCACGTTCTCTATCTATGTTGGTGATCGCTGTCACCATACCTCATCTTCTCAAGTGC 578
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140
DB 579 AAAGACAAAGTGAATTTCTACAGAAACTGCACTGCTGCTGCCAGTCTGCGATGG 638
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
DB 639 ACCTCGTGATGTTCTATGTTGGTACCCCTGGTGTCTCCGGTATCGAATCATGAGGA 598
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
DB 699 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAAATC 758
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
DB 759 ATCACTATATAGTATCATTTTGTGATAGCCGTTGCTGTGATTCGTGTTCTTCAG 818
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
DB 819 GTCTTCATCATATTGTTGATGTTGCAGAGCTACGCACTCTTTACTATCCACAGAG 878
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
DB 879 TTCCTGGCTCAGCTGAAACCTATTATTTATAGGGGTCACTCTGTTGTTCTTCCTCC 938
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
DB 939 TACCAGTCTCTTAGGATCTATTACTTGAATGTTGTGACCACTTCCATGCTGTAAACAG 998
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
DB 999 AAGGTTGCAATTTTATACGAAATCTTTCTTGAAGTTAACAGCAATTAGCTGATGATTTG 1058
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
DB 1059 CTCTCTCTTGTCTTTGGGGAGCCATTTGTTTAAACAAAGATAATTCGCTTATGGAT 1118
QY 301 CysValLeuCysArg 305
DB 1119 TGTGTTTGTGCGGT 1133
RESULT 8
ID AAF88584 standard; cDNA; 1340 BP.
XX AAF88584;
AC AAF88584;
XX 19-NOV-2002 (first entry)
XX Human GCREC-5 cDNA INCYTE ID 90012586CD1 SEQ ID 53.
XX GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
XX cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
XX cerebrotropic; antiinflammatory; virucide; antibacterial; fungicide;
XX protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
XX Parkinson's disease; Crohn's disease; constipation; infection;
XX gene therapy; gene; ss.
XX Homo sapiens.
XX WO200263004-A2.
XX 15-AUG-2002.
```

```
XX 06-FEB-2002; 2002WO-US003635.
XX 07-FEB-2001; 2001US-0267322P.
PR 23-FEB-2001; 2001US-0271215P.
PR 08-MAR-2001; 2001US-0274551P.
PR 23-MAR-2001; 2001US-0278507P.
PR 30-MAR-2001; 2001US-0280597P.
PR 02-APR-2001; 2001US-0281107P.
PR 06-APR-2001; 2001US-0282121P.
XX (INCY-) INCYTE GENOMICS INC.
PA Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;
XX Kallick DA, Gandhi AR, Wallia NK, Arvizu C, Elliott VS, Hafalia AJA;
PI Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DM;
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
PI Warren BA, Yang J, Lee EA, Harland L;
XX WPI; 2002-627557/67.
DR P-PSDB; AAB71326.
XX New human G-protein coupled receptors (GCREC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT over expression of functional GCRECs e.g. cancer, Alzheimer's and
PT Parkinson's.
XX Claim 114; Page 213; 239pp; English.
XX This invention describes novel polypeptides which have anti-HIV,
XX antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,
XX hepatotropic, laxative, cerebrotropic, antiinflammatory, virucide,
XX antibacterial, fungicide and protozoacide activity. The products of the
XX invention are useful for treating a disease or condition associated with
XX decreased expression or over expression of functional G-protein coupled
XX receptors (GCREC), while antibodies generated against the polypeptide of
XX the invention are useful for diagnosing a condition or disease associated
XX with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,
XX stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
XX constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
XX The compounds described in the invention can be used for gene therapy.
XX AAF88580-AAF88627 encode the GCREC proteins represented by AAB71322-
XX AAB71369, described in the disclosure of the invention
SQ Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.15e-128 Length: 1340
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-055-106C-2 (1-305) x AAF88584 (1-1340)
QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
DB 223 ATGCCTG3CCACAATACCTCCAGGAATTCCTTTGCGATCCTATAGTGACACCCACTTA 282
QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 283 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGTGTCATTTCCATCTTTTC 342
QY 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
DB 343 CTCCTGGTGAATGAACACCCGCTCAGTGACACCATGGCGGTCAATTAACCTTGGTGTG 402
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLeuThr 80
DB 403 GTCCACAGCGTTTTTCTGCTGACAGTGCCTATTTGCTTGACCTACCTCATCAAGAGACT 462
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
```

DB 180 CTCCTGGTGAATGAACACCGCGTCAGTGACCCACCATGGCGGTCAATTAACATGGTGGTG 239
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleValysThr 80
DB 240 GTCCACACGCTTTTCTCTGACAGTGCATTTGCTTGACCTACCTACCTCATCAAGAAGACT 299
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
DB 300 TGGATGTTTGGCTGCCCTTCTGCAAAATTTGAGTGCATGCTGCACATCCACATGTAC 359
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
DB 360 CTCACGTTCTCTATTCTATGTGTGTGATCTCTGTCACCATGATACCTCATCTTCTCAAGTGC 419
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLysSerAlaGlyMetTyr 140
DB 420 AAAGCAAGTGGAAATTTCTACAGAAACTGATGCTGTGGTGCAGCTGGCATGTGG 479
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
DB 480 ACGCTGGTGATTGTCTATGTGTGATCCCTGCTGTCTCCCGTATGGAATCCATGAGAA 539
QY 161 TyrAsnGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValysIle 180
DB 540 TACAATGAGGACACTGTTTAAATTTTCAAGAGCTTGCTTACACATATGTGAAAATC 599
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
DB 600 ATCAACTATATGATGATGATCTTTTGTATAGCCGTTGCTGTGATTCGTGTCTCCAG 659
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
DB 660 GTCTTCATCATATTGTTGATGGTGAGAGCTAGCCCACTCTTTACTATCCACAGGAG 719
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
DB 720 TCTGGGCTCAGCTGAAAACCTATTTTATAGGGTCACTCTTGTGTTCTTCCC 779
QY 241 TyrGlnPhePheArgIleTyrTrpLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
DB 780 TACCAGTCTCTTAGGATCTATTACTTGAATGTTGTGACGCAATTCATGCTGTAAACAGC 839
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
DB 840 AAGGTGCAATTTTATACCAATATTTCTTGAGTGTACAGCAATGAGCTGCTATGATTG 899
QY 281 LeuLeuPheValPheGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
DB 900 CTTCCTTTGTTCTTTGGGGGAAGCATTTGTTTAAAGCAAAAGATAAATGGCTTATGGAAT 959
QY 301 CysValLeuCysArg 305
DB 960 TGTGTTTGTCCCGT 974

RESULT 7

AAF88583
ID AAF88583 standard; cDNA; 1336 BP.

AC AAF88583;

DT 19-NOV-2002 (first entry)

DE Human GCREC-4 cDNA INCVTE ID 90012430CD1 SEQ ID 52.

XX GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
KW cystostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
KW cerebrotropic; antiinflammatory; virucide; antibacterial; fungicide;
KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
KW Parkinson's disease; Crohn's disease; constipation; infection;
KW gene therapy; gene; ss.

XX Homo sapiens.

OS

XX WO200263004-A2.
PX 15-AUG-2002.
XX 06-FEB-2002; 2002WO-US003635.
XX 07-FEB-2001; 2001US-0267322P.
PR 23-FEB-2001; 2001US-0271215P.
PR 08-MAR-2001; 2001US-0274551P.
PR 23-MAR-2001; 2001US-0278507P.
PR 30-MAR-2001; 2001US-0280597P.
PR 02-APR-2001; 2001US-0281107P.
PR 06-APR-2001; 2001US-0282121P.
XX (INCY-) INCVTE GENOMICS INC.
XX Baughn WR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;
PI Kallick DA, Gandhi AK, Wallia NK, Arvizu C, Elliott VS, Hafalia AJA;
PI Ramkumar J, Pei J, Tang Y, Yue H, Reddy R, Butford N, Lu DAM;
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
PI Warren BA, Yang J, Lee EA, Harland L;
XX MPI; 2002-627557/67.
DR P-PSDB; AAB71325.
XX New human G-protein coupled receptors (GCREC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT over expression of functional GCRECs e.g. cancer, Alzheimer's and
PT Parkinson's.
XX Claim 113; Page 212-213; 239pp; English.
XX This invention describes novel polypeptides which have anti-HIV,
CC antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,
CC hepatotropic, laxative, cerebrotropic, antiinflammatory, virucide,
CC antibacterial, fungicide and protozoacide activity. The products of the
CC invention are useful for treating a disease or condition associated with
CC decreased expression or over expression of functional G-protein coupled
CC receptors (GCREC), while antibodies generated against the polypeptide of
CC the invention are useful for diagnosing a condition or disease associated
CC with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,
CC stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
CC The compounds described in the invention can be used for gene therapy.
CC AAF88580-AAF88527 encode the GCREC proteins represented by AAB71322-
CC AAB71369, described in the disclosure of the invention
XX SQ Sequence 1336 BP; 340 A; 289 C; 287 G; 420 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.15e-128 Length: 1336
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-055-106C-2 (1-305) x AAF88583 (1-1336)
QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
DB 219 ATGCCTGGCCACAAATACCTCCAGGAATTCCTTGGATCCTATATGACCCCACTTA 278
QY 21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
DB 279 ATCAGCTCTACTTCAATAGTCTTATGGCGGCTGGTGGGTGCTATTCCTTCCTTC 338
QY 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
DB 339 CTCCTGGTGAATAATGAACACCCGGTCAGTGACCACTGCGGTCAATTAACCTGGTGGTG 398
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysThr 80

QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
 DB 121 CTCCTGGTGAATGAAACACCGGTCAGTGACCACTGGGGTCATTAACTTGGTGGT 180
 QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
 DB 181 GTCCACAGCGTTTCTGTCGACGTGCGCATTTGCTTGACCTACCTCATCAAGAAGACT 240
 QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
 DB 241 TGGATGTTTGGCTGCCCTTCTGCAAAATTTGAGTGCATGCTGCACATCCATGATGAC 300
 QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
 DB 301 CTCACGTTTCTATTCTATGTGGTGATCTCTGGTCAACAGATACCTCATCTTCTCAAGTGC 360
 QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAspAlaGlyMetTrp 140
 DB 361 AAAGCAAGTGGAAATTTACAGAAATTCGATGCTGGTGGCCAGTGGCATGGATGGG 420
 QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
 DB 421 ACGCTGGTGATGTGATGTGGTACCCCTGGTGTCTCCCGTATGGAATCCATGAGGAA 480
 QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
 DB 481 TACAAATGAGGACACTGTTTAAATTTACAAAGAGCTTGCTTACACATATGTGAAATC 540
 QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
 DB 541 ATCAACTATATGATAGTATGATTTTGTGATAGCGGTGCTGTGATTTCTTGGTCTTCCAG 600
 QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
 DB 601 GTCTTCATCATATGATGTGGTGCAGAGCTACGCCACTCTTTACTATATCCACAGAG 660
 QY 221 PheTrpAlaGlnLeuLysAsnLeuPheIleGlyValIleLeuValCysPheLeuPro 240
 DB 661 TTCGGGCTCAGCTGAAACCACTATTTTATAGGGTCACTCTGTTGTTCTTCTTCCC 720
 QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
 DB 721 TACCAGTCTTTTAGGATCTATTACTTGAATGTGTGACGCCATTCCAATGCCGTGAACAGC 780
 QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
 DB 781 AAGGTTCATTTTATAACGAAATCTTCTTGAGTGPACAGCAATTAGCTGCTATGATTG 840
 QY 281 LeuLeuPheValPheGlyCysSerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
 DB 841 CTTCTCTTTGCTTTGGGGAGCCATTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
 QY 301 CysValLeuCysArg 305
 DB 901 TGTGTTTGTGGCGT 915
 RESULT 5
 AAL57070
 ID AAL57070 standard; DNA; 1040 BP.
 XX
 AC AAL57070;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Human G-protein coupled receptor GAVE18 DNA sequence.
 KW Human G-protein coupled receptor; GAVE18; signal transduction;
 KW inflammation; physiological immunological response; antiinflammatory;
 KW antiasthmatic; antirheumatic; antiarthritic; antitense therapy;
 KW chromosomal mapping; tissue typing; forensic biology;
 KW predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;
 KW rheumatoid arthritis; gene; ds.

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..918
 FT /*tag= a
 FT /product= "GAVE18 protein"
 XX
 FN WO2003042399-A2.
 XX
 PD 22-MAY-2003.
 XX
 PF 08-NOV-2002; 2002WO-US035887.
 XX
 PR 13-NOV-2002; 2001US-0354150P.
 PR 22-MAR-2002; 2002GB-00006891.
 XX
 PA (AVET) AVENTIS PHARM INC.
 XX
 PI Eisingndrelo H, Cai J, Busch SJ, Gassenhuber J;
 XX
 DR WPI; 2003-457496/43.
 DR P-PSDB; AAO27265.
 XX
 FT New GAVE18 polypeptide and nucleic acid molecule encoding the
 PT polypeptide, useful for preventing and treating a disease or disorder
 PT associated with aberrant expression or activity of GAVE18, e.g. asthma or
 FT rheumatoid arthritis.
 XX
 PS Claim 1; Fig 5; 88pp; English.
 XX
 CC This invention relates to a novel G-protein coupled receptor (GAVE18)
 CC that is involved in signal transduction in respect to inflammation and
 CC the physiological immunological response. Molecules which may modulate
 CC the signalling activity or signal transduction of the receptor may be
 CC antiinflammatory, antiasthmatic, antirheumatic or antiarthritic. The
 CC GAVE18 receptor and the DNA sequence encoding it may be a target for
 CC antisense therapy or gene therapy. The nucleic acid molecule, GAVE18
 CC proteins and antibodies may be useful in screening assays, detection
 CC assays (for example chromosomal mapping, tissue typing or forensic
 CC biology), or predictive medicine (for example diagnostic assays.
 CC prognostic assays, monitoring clinical trials and pharmacogenomics. The
 CC nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse
 CC agonist and antagonist are also useful for preventing and treating a
 CC disease or disorder associated with aberrant expression or activity of
 CC GAVE18, such as inflammation and immunological-related diseases or
 CC disorders, for example asthma, chronic obstructive pulmonary disease or
 CC rheumatoid arthritis. The present sequence is the DNA sequence encoding
 CC the GAVE18 protein of the invention
 XX
 SQ Sequence 1040 BP; 289 A; 216 C; 213 G; 322 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8,65e-129 Length: 1040
 Score: 1532.00 Matches: 305
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-055-106C-2 (1-305) x AAL57070 (1-1040)

QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
 DB 1 ATGCCTGGCCACAATACCTCCAGAAATTCCTCTTGGATCCTATAGTACACCCCACTTA 60
 QY 21 ILSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
 DB 61 ATCAGCTCTACTTTCATAGTCTTATTTGGCGGCTGGTGGGTGTCAATTCATCTTTTC 120
 QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
 DB 121 CTCCTGGTGAATGAACACCCCGGTGAGTACACCATGCGGTCACTTAACCTTGGTGGTG 180

DB: 6 Gaps: 0
US-10-055-106C-2 (1-305) x ABZ59171 (1-918)
QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTGGGATCCTATAGTACACCCACCTTA 60
QY 21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db 61 ATCAGCCTCTACTTCATAGTGTATTTGGGGGCTGGTGGGTGTCATTTCCTATTCTTTTC 120
QY 41 LeuLeuValIysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 121 CTCCTGGTGAATGAAACACCCGGTCAGTGACCACTGGCGGTCAATTAACCTGGTGGT 180
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrIleLeuIleIysIysThr 80
Db 181 GTCCACAGCGTTTTTCTGTCAGAGTGCATTTTCGCTTACCTTACCTCATCAAGAGACT 240
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetIleHisIleHisMetTyr 100
Db 241 TGGATGTTGGGTGGCTCTGCAATTTGTGAGTGCCATGTCGACATCCACATGATGAC 300
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleLeuIlePhePheIysCys 120
Db 301 CTCACGTTCTATTATGTATGTGTGATCTGTCACCAAGATACCTCATCTCTTCAAGTGC 360
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140
Db 361 AAGACAAAGTGAATTTCTACAGAAACTGTCATGCTGGTGGCCAGTCTGGCATGTGG 420
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 421 ACCTGGTGAATGTCATTGTGGTACCCCTGCTGTCTCCGGTATGGAATCCATCAGGAA 480
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValIle 180
Db 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAGAGCTTGTCTTACACATATGTGAATTC 540
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 541 ATCACTATATATGATGATCTTTTGTATGATGATGATGATGATGATGATGATGATGAT 600
QY 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 601 GTCTTCATCATATTATGTGTGTGTCAGAGCTACGCCACTCTTTTACTATCCCAAGGAG 660
QY 221 PheTyrAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 661 TTCTGGCTCAGCTGAAACACCTATTTTATAGGGGTGTCATCTTCTTTGTTTCTTCC 720
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 721 TACCAGTCTCTTATAGGATCTATTACTTGAATTTGTGAGCGCATTCCTTCAATGCTTAC 780
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 781 AAGTTGCAATTTTATACGAAATCTCTTGTGAGTGTAAACGAATTAAGTCTATGATTTG 840
QY 281 LeuLeuPheValPheGlyGlySerHisTyrPheLysGlnLysIleLeuGlyLeuTyrAsn 300
Db 841 CTCTCTCTTCTCTTGGGGGAGCCATTTGTTTAAAGCAAGATAATTTGGCTTATGGAAT 900
QY 301 CysValLeuCysArg 305
Db 901 TGTGTTTGTGGCGT 915
RESULT 4
ID ABZ59171
XX ABZ59171 standard; DNA; 918 BP.
AC ABZ59171;

XX 28-APR-2003 (first entry)
XX Human TGR343 protein encoding DNA.
XX G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;
KW TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotropic;
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;
KW immunosuppressive; antiinflammatory; gene; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 1.918
CDS /*tag= a
FT /product= "TGR343"
FT
XX WO2003004678-A2.
XX 16-JAN-2003.
XX 01-JUL-2002; 2002WO-US020860.
XX 03-JUL-2001; 2001US-0302800P.
XX (TULA-) TULARIK INC.
XX Tian H, Dai K, Chen J, Zhao J, Cutler G;
XX WPI; 2003-210368/20.
XX P-PSDB; ABP71378.
XX New G-protein coupled receptor polypeptides designated TGR2, TGR38,
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or
PT nephrolithiasis.
XX Claim 7; Page 61; 74pp; English.
XX The invention provides new G-protein coupled receptor (GPCR) polypeptides
CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding
CC polynucleotides. The polypeptides can be expressed by standard DNA
CC recombination methodology. The polypeptides are useful for screening or
CC identifying modulation of GPCR or signal transduction. The modulators of
CC signal transduction are useful for treating or preventing TGR-associated
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The
CC polypeptides are useful as targets for diagnosing or treating e.g.
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia,
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,
CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute
CC inflammatory dermatoses. The present sequence represents a human TGR343
XX protein encoding DNA
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 7.52e-129 Length: 918
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-10-055-106C-2 (1-305) x ABZ59171 (1-918)
QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTGGGATCCTATAGTACACCCACCTTA 60
QY 21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db 61 ATCAGCCTCTACTTCATAGTGTCTTATTGGCGGGTGGTGGGTGTCATTTCCTATTCTTTTC 120

CC Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA
 CC libraries from peripheral blood mononuclear cells. Two ESTs have been
 CC identified in libraries derived from breast mRNA. PFI-021 and the
 CC corresponding cDNA are used to treat a patient needing altered activation,
 CC or expression of a GPCR, such as inflammation, allergy and respiratory,
 CC neurology, psychology, urogenital disease, reproductive and sexual
 CC dysfunction/disorders, cancer, tissue repair, dermatology, skin
 CC pigmentation disorders, photoaging, frailty, osteoporosis, metabolic
 CC disease, cardiovascular disease, gastro-intestinal disease, anti-
 CC infection, sensory organ disorders, sleep disorders and hair loss
 XX
 SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 7,52e-129 Length: 918
 Score: 1592.00 Matches: 305
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-055-106C-2 (1-305) x ABA00160 (1-918)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
 DB 1 ATGCTGGCCCAATACCTCCAGGAATTCCTTCGGATCCTATAGTGACACCCACTTA 60
 QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
 DB 61 ATCAGCCCTACTTCTCATAGTGTCTATTGGCGGCTGTGGTGTCAATTCCTATTC 120
 QY 41 LeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuVal 60
 DB 121 CTCCTGGTGAATGAACACCGGTCAGTACCCACCTGGCGGTCAATTAATTCCTGTG 180
 QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
 DB 131 GTCCACAGGGTTTCTCTGACAGTGCCTATTCCTGCTGACCTCATCAAGAGACT 240
 QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
 DB 241 TGGATGTTTGGCTGCCCTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCATGTAC 300
 QY 101 LeuThrPheLeuPheTyrValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
 DB 301 CTCAGTTCCTATCTATGTGGTGATCTGTGCACAGATACCTCATCTTCTCAAGTGC 360
 QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLaserAlaGlyMetTrp 140
 DB 361 AAAGACAAAGTGAATCTACAGAAACTGCAATGCTGTGGTGCAGTGCCTGGCATGTGG 420
 QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
 DB 421 ACGCTGGGATGTGATGTGTGATCCCTGCTGTCTCCCGATGGATCATCAGAGAA 480
 QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
 DB 481 TACATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTCTACACATATGTGAAATC 540
 QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
 DB 541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTGTGTGTGATCTCTGCTTCACG 600
 QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
 DB 601 GTCITCATCATATGTTGATGTGTGAGAGCTAGCCACTCTTTACTATCCACAGGAG 660
 QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
 DB 661 TTCTGGGCTCAGCTGAAACACCTATTTTATAGGGGTCACTCTGTGTTTCTCTCC 720
 QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260

DB 721 TACCAGTCTTTAGGATCTATTACTTGAATGTTGTGAGCGCATTCACATCCCTGTACAGC 780
 QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
 DB 781 AAGTTGCAATTTTATACCGAATCTCTTGTAGTGTACAGCAATTAGCTGCTATGATTG 840
 QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
 DB 841 CTTCCTCTTGTCTTCTGGGGAAGCCATTGTTTAAAGCAAAAGATAATTCCTTATGGAAT 900
 QY 301 CysValLeuCysArg 305
 DB 901 TGATTTTGTGCGGT 915

RESULT 3
 ABT04867
 ID ABT04867 standard; cDNA; 918 BP.
 AC ABT04867;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Human G protein coupled receptor hRUP29 coding sequence.
 XX
 KW Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
 KW hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200242461-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 26-NOV-2001; 2001WO-US044386.
 XX
 PR 27-NOV-2000; 2000US-0253404P.
 PR 12-DEC-2000; 2000US-0255366P.
 PR 20-FEB-2001; 2001US-0270266P.
 PR 20-FEB-2001; 2001US-0270286P.
 PR 06-APR-2001; 2001US-0282032P.
 PR 06-APR-2001; 2001US-0282356P.
 PR 06-APR-2001; 2001US-0282358P.
 PR 06-APR-2001; 2001US-0282365P.
 PR 14-MAY-2001; 2001US-0290917P.
 PR 31-JUL-2001; 2001US-0309208P.
 XX
 PA (AREN-) ARENA PHARM INC.

XX Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
 XX WPI; 2002-566565/60.
 XX P-PSDB; ABJ04069.
 XX
 XX Novel endogenous and non-endogenous versions of G protein-coupled
 XX receptor useful for identification of candidate compounds as receptor
 XX agonists or antagonists for use as therapeutic agents.
 XX
 XX Claim 7; Page 56-57; 84pp; English.

XX The present invention provides the protein and coding sequences of
 XX several human G-protein coupled receptors (GPCRs). These can be used in
 XX the identification of candidate compounds as receptor agonists or inverse
 XX agonists having applicability as therapeutic agents. The present sequence
 XX is a GPCR coding sequence of the invention
 XX
 XX Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 7,52e-129 Length: 918
 Score: 1592.00 Matches: 305
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 25, 2004, 18:01:50 ; Search time 447 Seconds
(without alignments)
2898.859 Million cell updates/sec

Title: US-10-055-106c-2

Perfect score: 1592

Sequence: 1 MFGHTSRNSSCDPVTTPHL.....GGSHWFKQIKIWNVCVLCR 305

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cpn2.1/USPTO.spool/US10055106/runat.21042004.161131.26172/app.query.fasta_1.455
-DB=N_Geneseq.257Jan04 -QFMT=Eastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10055106 @CGN.1.1.470 @runat.21042004.161131.26172 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq.29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1592	100.0	918	AAL44713	Human tes
2	1592	100.0	918	ABA00160	PFI-021 c
3	1592	100.0	918	ABT04867	Human G p
4	1592	100.0	918	ABZ59171	Human TGR
5	1592	100.0	1040	AAL57070	Human G-p
6	1592	100.0	1051	ABX87351	Human CDN
7	1592	100.0	1336	Aaf88583	Human GCR
8	1592	100.0	1340	Aaf88584	Human GCR

9	1592	100.0	1460	6	AAP88585	Human GCR
10	1592	100.0	2525	4	AAS1009	Human nGP
11	1592	100.0	2525	6	ABS70242	DNA encod
12	1592	100.0	113306	9	ADC86554	Human GPC
13	1587	99.7	939	6	AAL53414	939 nt co
14	1587	99.7	1684	6	AAL53413	1684 nt c
15	1547	97.2	1499	6	AAD37670	Human G-p
16	1176	73.9	972	9	ADC12789	Human GPC
17	1141	71.7	810	9	ADB78584	Mouse G-p
18	674	42.3	447	4	AAS0979	Human nGP
19	674	42.3	447	6	ABS70212	DNA encod
20	538	33.8	897	7	ABZ23663	G protein
21	294	18.5	479	4	AAS6763	Human imm
22	250	15.7	1358	3	AAZ95038	Human G p
23	247	15.5	1014	4	AAD06501	Human CYS
24	247	15.5	1014	7	ABZ42532	Human CON
25	245	15.4	1119	9	ADB74248	Rat GPR34
26	245	15.4	1122	9	ADB74249	Rat GPR34
27	240	15.1	1578	2	AAV62388	Human 7-t
28	240	15.1	1578	2	AAV71117	CDNA enco
29	236	14.8	1125	9	ADB74251	Mouse GPR
30	232.5	14.6	1498	4	AAH47235	Human C-p
31	232.5	14.6	1498	4	AAH16527	Human CDN
32	232	14.6	1101	4	AAP81543	Pig LNC4
33	231.5	14.5	1077	4	AAF82359	Human G p
34	231.5	14.5	1077	4	AAF86985	Human nov
35	231.5	14.5	1077	4	AAF55101	Nucleotid
36	231.5	14.5	1077	4	ACC51022	Human bla
37	231.5	14.5	1104	7	AAD52811	Human Mow
38	231.5	14.5	1143	9	ADB74230	Human GPR
39	231.5	14.5	1146	2	AAV61053	Human CLO
40	231.5	14.5	1146	7	ABZ42812	Human G p
41	231.5	14.5	1164	4	AAD06508	Human CON
42	231.5	14.5	1402	6	AAS98046	Human DNA
43	231.5	14.5	1402	7	ABX76412	Lung canc
44	231.5	14.5	1402	7	ABX76202	Lung canc
45	231.5	14.5	1402	7	ABZ78126	Human can

ALIGNMENTS

RESULT 1

AAL44713

ID AAL44713 standard; DNA; 918 BP.

XX AAL44713;

XX 03-MAY-2002 (first entry)

Human testis originated G-protein coupled receptor TGR10 coding sequence.

Human; testis-originated G-protein coupled receptor; TGR10; inflammatory; cystostatic; immunomodulator; cardiac; neuroprotective; gene therapy; inflammation; nervous system disease; circulatory system disease; cancer; metabolic disease; immunological disease; gastrointestinal disease; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS i. 918

FT /*tag= a

FT /product= "TGR10"

XX WO200196567-A1.

XX PD 20-DEC-2001.

XX PF 14-JUN-2001; 2001WO-JF005061.

XX PR 15-JUN-2000; 2000JP-00184596.

XX PR 19-JUL-2000; 2000JP-00233887.

QY	141	ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu	160
Db	801	ACGCTGGTGATGTGTCATGTGTGTACCCCTGGTTGCTCCCGGTATGGAATCCATGAGGAA	860
QY	161	TyrAsnGluGluHisCysPheHisLysGluLeuAlaTyrThrTyrValIle	180
Db	861	TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC	920
QY	181	IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln	200
Db	921	ATCAACTATATATATGATGCTATTTTGTATAGCGGTGCTGTGATTCGTGGTCTTCCAG	980
QY	201	ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu	220
Db	981	GTCTTCATCATTTATGTGTGATGTGCAGAGCTACGCCACTCTTTACTATCCACCAGGAG	1040
QY	221	PheTyrAlaGlnLeuLysAsnLeuPheIleGlyValIleLeuValCysPheLeuPro	240
Db	1041	TTCTGGGCTCAGCTGAAACCTATTTTTTATAGGGTCATCCTTGTTGTTCTTCTCC	1100
QY	241	TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer	260
Db	1101	TACCAGTTCTTTAGGATCTATTACTTGAATGTGTGACGCATTCCAATGCCCTGTAAACAGC	1160
QY	261	LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAsnLeu	280
Db	1161	AAGGTGTCATTTTATAACGAATCTTCTTGAGTGTAAACAGCAATTAGCTGCTATGATTG	1220
QY	281	LeuLeuPheValPheGlyGlySerHisTyrPheLysGlnLysIleIleGlyLeuTyrAsn	300
Db	1221	CTTCTCTTTGTCTTTGGGGAGGCCATTGGTTTAAAGCAAAGATAAT-GGCTTATGGAAT	1279
QY	301	CysValLeuCysArg	305
Db	1280	TGTGT-TTGTGCCGT	1293

Search completed: April 25, 2004, 21:29:30
Job time : 4525 secs

```
misc_feature 24986..66573
/notes="assembly_name:Contig4"
misc_feature 66574..164055
/notes="assembly_name:Contig5"

ORIGIN
Alignment Scores:
Pred. No.: 1.41e-107 Length: 164055
Score: 1579.00 Matches: 303
Percent Similarity: 99.34% Conservatives: 0
Best Local Similarity: 99.34% Mismatches: 2
Query Match: 99.18% Indels: 0
DB: 2 Gaps: 0

US-10-055-106C-2 (1-305) x AC146385 (1-164055)

QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
DB 16121 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGCATCCTATAGTACACCCCACTTA 16062

QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
DB 16061 ATCAGCCTCTACTTCATAGTGCTCATTTGGGGGCTGGTGGTGCATTTCCATCTTTTC 16002

QY 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
DB 16001 CTCCTGGTGAATAATGAACCCGCTCAGTGACCACCATGGCGGTCAATTAACCTTGGTGGTG 15942

QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
DB 15941 GTCCACAGCGTTTCTGCTGACAGTGCCATTTGCTTGACCTACCTCATCAGAGAGACT 15882

QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
DB 15881 TGGATGTTTGGGCTGCCCTCTCTGCAAAATTTCTGAGTGCCATGCTGCACATCCACATGTAC 15822

QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
DB 15821 CTCACGTTCTATCTAAGTGGATCCTGTCACAGATACCTCACTTCTTCTCAAGTGC 15762

QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLysAlaSerAlaGlyMetTrp 140
DB 15761 AAAGACAAAGTGGAAATCTACAGAAACTGCATGCTGTGGCTGCCAGTGGCATGTGG 15702

QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
DB 15701 ACCTGGTGTATGTCTATGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 15642

QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
DB 15641 TACAAAGAGGACACTGTTTACATTTTCAAAAGAGCTTCTTACACATATGTGAAATC 15582

QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
DB 15581 ATCAACTATATATGATGATCAATTTTGTATAGCCGTTGCTGTGATCTGTTGGTCTTCCAG 15522

QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
DB 15521 GTCTTCATCATATGTTGATGGTGCAGAGCTACGCCACTCTTACTATCCACACAGGAG 15462

QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
DB 15461 TTCTGGGCTCAGCTGAAAAACCTATTTTTATAGGGGTGCATCTGTTGTTCTTCTTCCC 15402

QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
DB 15401 TACCAGTCTTTAGGATCTAATTAAGTGTGTGAGCGATTCATTCATGCTGTACAGC 15342

QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
DB 15341 AAGGTTGCAATTTATACGAAATCTTCTGAGTGTACAGCAATAGCTCTATGATTTG 15282

QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
```



```
----- 1306 1313 1358 1406 8347 8084
----- 374 <800 2400 2394 3636 3640
-----

Alignment Scores:
Pred. No.: 1,97e-108 Length: 218186
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-055-106c-2 (1-305) x AC083865 (1-218186)
QY 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
DB 133123 ATGCGTCGGCCACAATACCTCCAGGAATCTCTTGGATCCTATAGTGACACCCACATTA 133182
QY 21 IleSerLeuTyPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
DB 133183 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGCTGGTGGGTGCATTTCCTATTCTTTC 133242
QY 41 LeuLeuValIleMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
DB 133243 CTCCTGTGAAATGAATGAACCCCGGTGAGTGCACCATCCGCGTCAATAACTTGGTGGTG 133302
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyLeuIleLeuLysLysThr 80
DB 133303 GTCCACAGCGTTTCTGCTGACAGTGCCATTTCGCTTGACCTACTCATCAAGAAGACT 133362
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
DB 133363 TGGATGTTTGGGCTGCCCTCTGCAATTTGTGAGTGCCATGTCACATCCACATGTAC 133422
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
DB 133423 CTCACGTTCTCTATTCTATGTTGGTGATCTCTGTCACCATACCTCATCTTCTTCAAGTGC 133482
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140
DB 133483 AAAGACAAAGTGAATTTCTACAGAAACTGCATGCTGTGGCTGCCAGTCTGCGCATGTGG 133542
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
DB 133543 ACCCTGGTGATTTGATTTGTTGGTACCCCTGGTTGTCTCCGGTATGGATTCATCAGGNA 133602
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
DB 133603 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC 133662
QY 181 IleAsnTyMetIleValIlePheValIleAlaValAlaValIleLeuValPheGln 200
DB 133663 ATCAACTATATGATGATCATTTTGTGATAGCGGTTGCTGTGATTCGTGTCTTCCAG 133722
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
DB 133723 GTCTTCATCATATTGTTGATGGTGAGAGCTAGCCACTCTTACTATCCACAGGAG 133782
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
DB 133783 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTGCATCTGTTGTTCTTCTTCC 133842
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
DB 133843 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAAACAG 133902
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
DB 133903 AAGGTTGCAATTTTATAACGAAATCTTCTTGAGTGTAAACGCAATAGCTGCTATGATTTG 133962
QY 281 LeuLeuPheValPheGlyGlySerHisTyrPheLysGlnLysIleIleGlyLeuTyrAsn 300
```

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

ECORI

HindIII

BglII

SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt
8696	8979	764	755	3414	3439
6	<800	6382	6611	2067	2102
663	<800	512	<800	5356	5585
122	<800	449	<800	1416	1421
174	<800	1059	1063	610	<800
4551	4612	70	<800	225	<800
952	988	424	<800	932	961
968	988	2594	2670	1982	2102
980	988	3852	3908	29	<800
10043	10231	915	918	2663	2719
2412	2471	5333	5315	5958	5921
3670	3625	4795	4869	448	<800
4365	4323	668	<800	8190	8084
27	<800	552	<800	1869	1948
9749	10231	1010	1063	3655	3640
703	<800	884	918	14842	14314
1957	2017	2280	2278	3924	3962
2403	2471	4595	4869	591	<800
9	<800	654	<800	1362	1270

359	<800	2624	2670	572	<800
57	<800	13428	13500	2139	2102
2128	2184	12540	12591	1593	1527
1087	1101	4819	4869	2049	2102
2839	2805	11280	11329	614	<800
2787	2805	840	918	7901	8084
5407	5309	9244	8985	619	<800
3324	3348	1672	1707	5583	5585
7246	7468	3195	3163	345	<800
4508	4455	4273	4301	324	<800
5815	5686	1980	2031	1496	1421
5380	5309	520	<800	6710	6637
349	<800	737	755	71	<800
4509	4612	1833	1878	848	877
571	<800	8798	8985	6153	6135
4162	4455	2024	2031	4085	4113
956	988	4946	4869	14	<800
2026	2123	6247	6163	44	<800
1821	1788	685	<800	10402	10380
2453	2471	1367	1406	300	<800
8955	9499	109	<800	5150	5294
1004	988	3608	3535	3195	3246
7399	7468	7728	7736	2281	2309
7516	7468	4264	4301	2740	2804
4119	4107	357	<800	5869	5921
193	<800	3645	3709	248	<800
2792	2805	1961	2031	3072	3079
7034	7468	5668	5588	585	<800
4940	4902	957	918	655	<800
603	<800	5024	4869	1206	1270
761	<800	201	<800	1723	1693
2518	2471	1119	1195	19721	20141
4086	4107	709	<800	2331	2309
5916	5835	4907	4869	1940	1993
6995	6947	1161	1195	5574	5585
4667	4612	11292	11329	3867	3865
10434	10231	6699	6611	1268	1270

```
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
join(201..207,11526..12452,37954..38097,98732..98784,
112891..113106)
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD69533.1"
/db_xref="GI:28793226"
/translation="MTGDFPSMPGHTSRNSCDPIVTHLISLVFVLIGLVGVIS
ILFLVQMTFRVTVAVNLVHVSFLVFLRLTYLIKKTWVGLPFCFKFSAML
HLMVLTQVTVLVVLIFFKCKDKVEFKLHVAASAGMTLVIVIVPLVWS
RGIHEEYNEECFPHKELAVYKINMIVIVIAVAVILLVQVFIIMLVQKL
RSLASHQFMAQLNRLPFLGVLVLCFLPYOPFIYVILNVVTHSNACNKAIFYNEIF
LSVTAISCVDLLLFVGGSHWFKOKIIGLWVCLGNPSGLTPCFQSLSLLEHLPAM
AGSVHCSVLRIGEVSRKCFELFRPRTDLCLEFNNHTYAKVBFRAVTKLESGTI
SAHCTLYLPDSNSPASASQVAGITGTHHAQLIFVLVETGFHVGQGLDLITS"
ORIGIN
Alignment Scores:
Pred. No.: 1,05e-108 Length: 113306
Score: 1922.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-055-106C-2 (1-305) x AX646815 (1-113306)
QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
Db 11540 ATGCCTGGCCACAAATACCTCCAGGAATCTCTTGGGATCCCTATAGTGACACCCACCTA 11599
QY 21 IleSerLeuTyPheIleValleuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db 11600 ATCAGCCTCTACTCTAGTGTCTATTGGGGGCTGGTGGGTGCTATTTCCATTTCTTTC 11659
QY 41 LeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 11660 CTCTGGTGAATAAGAACCCCGTCAGTGACCAACCATCGCGTCAATTAACCTGGTGGTG 11719
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrrLeuIleIleValSthr 80
Db 11720 GTCCACAGCGTTTTCTGTGACAGGCCATTCCTGGCTTACCTCATCAGAGACT 11779
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetIleHisIleMetTyrr 100
Db 11780 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGTCACATCCACATGTAC 11839
QY 101 LeuThrPheLeuPheTyrrValValIleLeuValThrArgTyrrLeuIlePhePheLysCys 120
Db 11840 CTCACGTTCTATCTATGATGGGTGATCCCTGGTCACAGATACCTCATCTTCTCAAGTGC 11899
QY 121 LysAspLysValGluPheTyrrArgLysLeuHisAlaValAlaSerAlaGlyMetTrp 140
Db 11900 AAGACAAAGTGAATCTACAGAAAATGCTGCTGGTGCAGTGTGCTGGCATGTGG 11959
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrrGlyIleHisGluGlu 160
Db 11960 ACCTGGTGTATGATGTTGGTACCCCTGGTGTCTCCCGGATGGAATCATGATGAGAA 12019
QY 161 TyrAsnGluGluHisCysPheLysPheHisIleGluLeuAlaTyrrThrTyrrValIle 180
Db 12020 TACAAAGAGAGACACTGTTTAAATTCACAAAGAGCTTGTACACATATGTGAATAATC 12079
QY 181 IleAsnTyrrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 12080 ATCAACTATATGATGATCAATTTTGTGCATAGCCGTTGCTGTGATTTCTGTGCTTCCAG 12139
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 12140 GTCTTTCATCATTAATGATGGTGAGAGACTAGCCACTCTTTACTATCCACACAGGAG 12199
```

```
221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
12200 TTCTGGGCTCAGGTGAATAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCCC 12259
QY 241 TyrGlnPhePheArgIleTyrrTyrrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
12260 TACCAGTCTCTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTGTAAACG 12319
QY 261 LysValAlaPheTyrrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrrAspLeu 280
12320 AAGTTTCATTTTATACGAAATCTCTTCTGAGTGTACAGCAATTAGCTGCTATGATTG 12379
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleLeuGlyLeuTrpAsn 300
12380 CTTCTCTCTTGTCTTGGGGGAAGCACTTGTCTTAAAGCAAAAGATAATTGGCTTATGGAAT 12439
QY 301 CysValLeuCysArg 305
Db 12440 TGTGTTTGTGCGCT 12454
RESULT 13
AC083865 218186 bp DNA linear PRI 26-JAN-2001
LOCUS Homo sapiens chromosome 7 clone RP11-605P22, complete sequence.
DEFINITION AC083865
ACCESSION AC083865.2 GI:12545315
VERSION AC083865.2
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 218186)
AUTHORS Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and Olson,M.V.
TITLE Large-scale Mapping and Sequencing of Human Chromosome 7
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 218186)
AUTHORS Kaul,R., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-2000) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 218186)
AUTHORS Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and Olson,M.V.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
COMMENT On Jan 26, 2001 this sequence version replaced gi:10567930.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgss@u.washington.edu
----- Project Information
Center project name: HsaChr7
Center clone name: RP11-605P22 (dj8708)
----- Summary Statistics
Sequencing vector: plasmid; X52328; 100% of reads
Chemistry: Dye-terminator Em-amersham; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 217693 bases at least Q40
Consensus quality: 218145 bases at least Q30
Consensus quality: 218186 bases at least Q20
Insert size: 273875; 19.1% error; agarose-fp
Insert size: 218186; sum-of-contigs
Quality coverage: 8.30x in Q20 bases; agarose-fp
Quality coverage: 10.42x in Q20 bases; sum-of-contigs
-----
Overlapping Sequences:
5': mapping in progress
3': RP11-243E12 (UWGC:djs156) AC018634, 6468-bp overlap
-----
```

Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValIleLeuLeuValPheGln 200
Db 567 ATCACTATATGATAGTCAATTTTGTCTAGCCGTTGCTGATTCCTGTTGGTCTTCAG 626
Qy 201 ValPheIleIleMetLeuMetValGlnIlyValLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 627 GTCTTCATCATTAAGTGGTGGAGAGAGTACGCCACTCTTACTATCCACACAGAG 686
Qy 221 PheTrpAlaGlnLeuLeuAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 687 TTCTGGGTCAGTCGAAACCACTATTTTATAGGGTCACTCTTGTGTTCTTCCTCC 746
Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 747 TACCAGTCTCTTAGGATCTTACTTGAATGTTGTGACGCAATTCATGCTGTAAACAGC 806
Qy 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 807 AAGGTTGCATTTTATAACGAAATCTTCTGTAGTGTAAACAGCAATTAGCTGTATGATTG 866
Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheGlyGlnIlyValIleGlyLeuTrpAsn 300
Db 867 CTCTCTCTTGTCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 926
Qy 301 CysValLeuCysArg 305
Db 927 TGTGTTTGTGCGGT 941
RESULT 11
AX521885 2525 bp DNA linear PAT 24-OCT-2002
LOCUS Sequence 81 from Patent WO02064789.
DEFINITION AX521885
ACCESSION AX521885.1 GI:24410791
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lind, P., Parodi, L.A., Vogeli, G. and Wood, L.S.
TITLE G protein-coupled receptor
JOURNAL Patent: WO 02064789-A 81 22-AUG-2002;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
source
1. .2525
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 2,71e-110 Length: 2525
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-055-106C-2 (1-305) x AX521885 (1-2525)
Qy 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 27 ARGCTGGCCCAAACTCCAGGAATTCCTCTTCGGATCCCTATAGTGACACCCACCTTA 86
Qy 21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db 87 ATCAGCCTCTACTTCATAGTGTATTTGGGGCTGGTGGGTGCTCATTTCCATTTCTTC 146
Qy 41 LeuLeuValIlyMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 147 CTCCTGGTGAAATGAACACCCGGTCAGTGACACCCAGTGGCGGTCTTAATTCGTGGTG 206

Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleIlyValThr 80
Db 207 GTCACAGCGGTTTTCTGCTGACAGTGCCATTTGCTTGACCTACCTCACTCAAGAGACT 266
Qy 81 TrpMetPheGlyLeuProPheCysIlyPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 267 TGGATGTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 326
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheCysCys 120
Db 327 CTCACGTTCTATTCATGTGGTATCCTGGTCACAGATACCTCATCTTCITCAAGTGC 386
Qy 121 LysAspIlyValGluPheTyrArgIlyLeuHisAlaValAlaAlaSerAlaGlyMetTyr 140
Db 387 AAGACAAAGTGGAAATCTACAGAAATCGATGCTGTGCTGCCAGTGTGGCATGTGG 446
Qy 141 ThrLeuValIleValIleValValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 447 ACCTGCTGATTTGCTATTGTTGTTACCCCTGGTGTCTCCGGTATGGAATCCATGAGAA 506
Qy 161 TyrAsnGluGluHisCysPheIlyPheHisIlyValLeuAlaTyrThrTyrValIlyIle 180
Db 507 TACATGAGGAGACCTGTTTAAATTTTCAAAAGAGCTTGTCTACACATATGTGAAATC 566
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 567 ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATTTCTTGTGCTTCCAG 626
Qy 201 ValPheIleIleMetLeuMetValGlnIlyLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 627 GTCTTCATCATTAAGTGTGAGTGGAGAGAGTACGCCACTCTTACTATCCACACAGAG 686
Qy 221 PheTrpAlaGlnLeuIlyAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 687 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTATCTCTTGTGTTCTTCTTCCC 746
Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAlaCysAsnSer 260
Db 747 TACCAGTCTCTTAGGATCTTACTTGAATGTTGTGACGCAATTCATGCTGTAAACAGC 806
Qy 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 807 AAGGTTGCATTTTATAACGAAATCTTCTGAGTGTAAACAGCAATTAGCTGTATGATTG 866
Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheGlyGlnIlyIleIleGlyLeuTrpAsn 300
Db 867 CTCTCTCTTGTCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 926
Qy 301 CysValLeuCysArg 305
Db 927 TGTGTTTGTGCGGT 941
RESULT 12
AX646815 113306 bp DNA linear PAT 04-MAR-2003
LOCUS Sequence 1007 from Patent EP1270724.
DEFINITION AX646815
ACCESSION AX646815.1 GI:28799225
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
TITLE Guanine triphosphate-binding protein coupled receptors
JOURNAL Patent: EP 1270724-A 1007 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
(JP) ; Center for Advanced Science and Technology Incubation, Ltd.
(JP)
FEATURES
source
Location/Qualifiers
1. .113306

ORIGIN		Db		1243		TGCTGTTTGTGCGCT		1257	
Alignment Scores:		RESULT 10		AXI47836		Sequence 81 from Patent WO0136473.		DNA	
Pred. No.:		1.6e-110		Length: 1460		2525 bp		linear	
Score:		1592.00		Matches: 305		Accession		PAT 08-JUN-2001	
Percent Similarity:		100.00%		Conservative: 0		AXI47836			
Best Local Similarity:		100.00%		Mismatch: 0		AXI47836			
Query Match:		100.00%		Indels: 0		VERSION			
DB:		6		Gaps: 0		AXI47836.1		GI:14346839	
US-10-055-106C-2 (1-305) x AX709195 (1-1460)		SOURCE		Homo sapiens (human)		KEYWORDS			
QY		1		MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu		ORGANISM		Homo sapiens	
DB		343		ATGCTGGCCACAAATACCTCCAGAAATTCCTCTGGATCCCTATAGTACACCCCACTTA		REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
QY		21		IleSerLeuThrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe		AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
DB		403		ATCAGGCTCTACTTCATAGTCTTATGGGGCTGGTGGTGTCTATTTCCATTTCTTTTC		TITLE		Vogeli, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P.,	
QY		41		LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal		JOURNAL		Sejltz, T. and Huff, R.M.	
DB		463		CTCCTGGTGAATATGAACCCCGTCCAGTACCCACCATGCGGTCTTAATCTGGTGGTG		FEATURES		Novel g protein-coupled receptors	
QY		61		ValHisSerValPheLeuLeuThrValProPheArgLeuThrThrLeuLeuLysThr		source		Patent: WO 0136473-A 81 25-MAY-2001;	
DB		523		GTCCACAGCGTTTTTCTGCTGACAGTGCCTATTCGCTTACCTCATCAAGAGACT		1. .2525		PHARMACIA & UPJOHN COMPANY (US)	
QY		81		TTPMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr		/organism="Homo sapiens"		Location/Qualifiers	
DB		583		TGGATGTTGGGTGGCTTCGCAAAATTTGTGAGTGCCATGTCACATCCACATGTAC		/mol_type="unassigned DNA"		1. .2525	
QY		101		LeuThrPheLeuPheThrValValIleLeuValThrArgThrLeuIlePhePheLysCys		/db_xref="taxon:9606"		0	
DB		643		CTCACGTTCTTATCTATGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG		Alignment Scores:		2.71e-110	
QY		121		LysAspLysValGluPheThrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyr		Pred. No.:		Length: 2525	
DB		703		AAGACAAAGTGAATTTCTACAGAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTG		Score:		Matches: 305	
QY		141		ThrLeuValIleValIleValProLeuValValSerArgThrGlyIleHisGluGlu		Percent Similarity:		Conservative: 0	
DB		763		ACGCTGGTGTATGCTATGTTGGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG		Best Local Similarity:		Mismatch: 0	
QY		161		TyrAsnGluGluHisCysPheLysPheHisGlyLeuAlaThrThrThrValLysIle		Query Match:		Indels: 0	
DB		823		TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTCTTACACATATGGAATTC		DB:		Gaps: 0	
QY		181		IleAsnThrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln		US-10-055-106C-2 (1-305) x AXI47836 (1-2525)			
DB		883		ATCAACTATATGATAGTCAATTTTGTGATAGCCGTTGCTGTGATTTCTGTTGGTCCAG		QY		1	
QY		201		ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu		DB		27	
DB		943		GTCTTTCATATATGTTGGTGGAGAGCTACGCCACTCTTTACTATCCACAGGAG		QY		21	
QY		221		PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro		DB		87	
DB		1003		TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTATCTGTTGTTTCTTCTCC		QY		41	
QY		241		TyrGlnPhePheArgIleThrThrLeuAsnValThrHisSerAsnAlaCysAsnSer		DB		147	
DB		1063		TACCAGTTCTTAGGATCTATTACTTGAATGTTGTGACGATTTCCAAATGGCTGTAAACAG		QY		61	
QY		261		LysValAlaPheThrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu		DB		207	
DB		1123		AAGTTTCATTTTATACGAAATCTTCTTGAGTGTACAGCAATAGCTGCTATGATTG		QY		81	
QY		281		LeuLeuPheValPheGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn		DB		267	
DB		1183		CTTCTCTTGTCTTGGGGAAGCAATGGTTTAAAGCAAAAGATAATTGGCTTATGGAAT		QY		101	
QY		301		CysValLeuLeuCysArg 305		DB		327	

```
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 939 TACCAGTTCCTTTAGGATCTATTACTTGAATGTGTGAGCGCATTCACATGCCCTGTAAACAGC 998
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 999 AAGGTTCGATTTTAAACGAAATCTTCTTGAGTGTACAGCAGATTTAGCTGTATGATTTG 1058
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleGlyLeuTrpAsn 300
Db 1059 CTTCTCTTGTCTTTGGGGAGACCATTTGGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 1118
QY 301 CysValLeuCysArg 305
Db 1119 TGTGTTTTGTGCCGT 1133

RESULT 8
AX709194 1340 bp DNA linear PAT 04-APR-2003
LOCUS AX709194
DEFINITION Sequence 53 from Patent WO02063004.
ACCESSION AX709194
VERSION AX709194.1 GI:29564788
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
LOCATION/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baughn,M.R., Tribouley,C.M., Nguyen,D.B., Thornton,M., Yao,M.G.,
Kallik,D.A., Gandhi,A.R., Walla,N.K., Arvizu,C., Elliott,V.S.,
Hafalia,A.J., Ramkumar,J., Pei,J., Tang,Y.T., Yue,H., Reddy,R.,
Burford,N., Lu,D.A., Graul,R.C., Khan,F.A., Walsh,R.T., Ison,C.H.,
Richardson,T.W., Griffin,J.A., Warren,B.A., Yang,J., Lee,E.A. and
Harland,L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 02063004-A 53 15-AUG-2002;
INCYTE Genomics, Inc. (US)
FEATURES
source 1..1340
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 90012586CB1"

ORIGIN
Alignment Scores:
Pred. No.: 1..47e-110 Length: 1340
Score: 1592.00 Matches: 305
Percent Similarity: 100.00 Conservative: 0
Best Local Similarity: 100.00 Mismatches: 0
Query Match: 100.00 Indels: 0
DB: 6 Gaps: 0

US-10-055-106C-2 (1-305) x AX709194 (1-1340)

QY 1 MetProGlyHisAsnThrSerArgLysSerCysAspProIleValThrProHisLeu 20
Db 223 ATGCCTGGCCACATACCTCCAGGAATTCCTTCGATCCTATAGTACACCCACATTA 282
QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 283 ATCACCTCTACTTCTATAGTGTCTTATGGGGCTGTGGGTGTCTATTCATCTTTC 342
QY 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 343 CTCCTGGTGAATGAACACCCGGTCAGTGACCATGGCGGTCAATTAACCTTGGTGTG 402
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
Db 403 GTCCACAGGCTTTTCTGCTGACGTGCATTTCCCTTGACCTACTCTATCAGAGACT 462
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
```

```
Db 463 TGGATGTTGGGCTGGCCTTCTCCTCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 522
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db 523 CTCAGTTCTCTATTTCTATGTGGTGATCCTGGTACCAGATACCTCATCTTCTTCAAGTGC 582
QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaIleSerAlaGlyMetTrp 140
Db 583 AAAGACAAAGTGAATTTCTACAGAAACGTCATGCTGTGGCTGCCAGTGTGCATGTGG 642
QY 141 ThrLeuValIleValIleValValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 643 AGCTGGTGATTTGTCATTTGGTACCCCTGGTTGTCTCCGGTATGGAATCCATGAGAA 702
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
Db 703 TACAATGAGGAGCAGCTGTTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 762
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 763 ATCACTATATGATGTCATTTTGTATAGCCGTGTGCTGTGATTTCTGTGGTCTTCCAG 822
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 823 GTCTTCATCATTTATGTTGATGTGTCAGAGCTACGCCACTCTTTACTATCCACCAGGAG 882
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 883 TTCGGGCTCAGCTGAAGAAACCTATTTTATAGGGTGCATCCTGTGTTGTTCTTCC 942
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 943 TACCAGTTCCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAATGCTGTAAACAGC 1002
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 1003 AAGTTGTCATTTTATACGAAATCTTCTTGAGTGTAAACAGCAATTAATGGCTTATGGAAT 1122
QY 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleGlyLeuTrpAsn 300
Db 1063 CTTCTCTTGTCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATGGCTTATGGAAT 1122
QY 301 CysValLeuCysArg 305
Db 1123 TGTGTTTTGTGCCGT 1137

RESULT 9
AX709195 1460 bp DNA linear PAT 04-APR-2003
LOCUS AX709195
DEFINITION Sequence 54 from Patent WO02063004.
ACCESSION AX709195
VERSION AX709195.1 GI:29564789
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
LOCATION/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baughn,M.R., Tribouley,C.M., Nguyen,D.B., Thornton,M., Yao,M.G.,
Kallik,D.A., Gandhi,A.R., Walla,N.K., Arvizu,C., Elliott,V.S.,
Hafalia,A.J., Ramkumar,J., Pei,J., Tang,Y.T., Yue,H., Reddy,R.,
Burford,N., Lu,D.A., Graul,R.C., Khan,F.A., Walsh,R.T., Ison,C.H.,
Richardson,T.W., Griffin,J.A., Warren,B.A., Yang,J., Lee,E.A. and
Harland,L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 02063004-A 54 15-AUG-2002;
INCYTE Genomics, Inc. (US)
FEATURES
source 1..1460
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 90012670CB1"
```

```

Db 120 ATCAGGCTCTACATGCTAGTGTATTTGGGGCTGGTGGTCTATTTCCATTTCTTTTC 179
Qy 41 LeuLeuVallyMetAenThrArgSerValThrMetAlaValIleAenLeuValVal 60
Db 180 CTCTCTGGTGAATGAAACACCCCGTCAGTGACACCATGGCGTCTATTAACCTTGGTGG 239
Qy 61 ValHisSerValPheLeuLeuThrValPropheArgLeuThrThrLeuLeuLysThr 80
Db 240 GTCCACAGCGTTTTCTGCTGACAGTGCATTTTCGCTTGACCTACCTCATCAAGAAGACT 299
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisLeuValThr 100
Db 300 TGGATGTTGGGCTGCCCTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCATGTAC 359
Qy 101 LeuThrPheLeuPheThrValValIleLeuValThrArgThrLeuLeuPhePheLysCys 120
Db 360 CTCACGTTCTTCTATGATGGTGATGCTGCTGCCAGATACCTCATCTTCTCAAGTGC 419
Qy 121 LysAspLysValGluPheThrArgLysLeuHisAlaValAlaLysAlaGlyMetThr 140
Db 420 AAAGACAAAGTGAATTTCTACAGAAACCTGCTGCTGGTCCCATGCTGGCATGTGG 479
Qy 141 ThrLeuValIleValIleValProLeuValValSerArgThrGlyIleHisGluGlu 160
Db 480 ACCTGGTGATGCTCATTTGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
Qy 161 TyrAsnGluHisCysPheLysPheHisLysGluLeuAlaThrThrThrValLysIle 180
Db 540 TACAATGAGGAGACACTGTTTTAAATTTCAAAAGAGCTTGCTTTACACATATGTGAAATC 599
Qy 181 IleAsnThrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 600 ATCAACTATATGATGCTCATTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
Qy 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 660 GTCTTCATCATTTATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
Qy 221 PheThrAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 720 TTCTGGGCTCAGCTGAAACCTATTTTATATAGGGGTATCTCTGTTGTTGTTCTTCTTCC 779
Qy 241 TyrGlnPhePheArgIleThrValLeuAsnValThrHisSerAsnAlaCysAsnSer 260
Db 780 TACCAGTCTCTTATGATCTATTAATCTGAAATGTTGTCAGCAATTCCTCAATGCTGTAACAG 839
Qy 261 LysValAlaPheThrAsnGluIlePheLeuSerValThrAlaIleSerCysThrPheLeu 280
Db 840 AAGTTGTCATTTTATACGAAATATCTTGTAGTGTAACCAATTAAGCTGCTGCTGCTGCT 899
Qy 281 LeuLeuPheValPheGlyGlySerHisThrPheLysGlnLysIleIleGlyLeuThrAsn 300
Db 900 CTCTCTTTGCTTTGGGGAGCCCATTTGTTTAAAGAAAGATAATTTGGCTTATGGAAT 959
Qy 301 CysValLeuCysArg 305
Db 960 TGTGTTTGTGGCGT 974

RESULT 7
AX709193
LOCUS 1336 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 52 from Patent WO2063004.
ACCESSION AX709193
VERSION AX709193.1 GI:29564787
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallick, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S.,

```

```

Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and
Harland, L.
G-protein coupled receptors
Patent: WO 02063004-A 52 15-AUG-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
1. 1336
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 90012430CE1"

```

FEATURES

source

ORIGIN

Alignment Scores:

```

Pred. No.: 1,47e-110 Length: 1336
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

```

US-10-055-106C-2 (1-305) x AX709193 (1-1336)

```

Qy 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 219 ATGCTGGCCCAATATCTCCAGGAATTCCTTTGGATCTATAGTGACACCCCATTTA 278
Qy 21 IleSerLeuThrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db 279 ATCAGCCTCTACTTCATAGTCTTATTGGCGGGCTGGTGGGTGCATTTCCATCTTTTC 338
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
Db 339 CTCCTGGTGAATAATGAACACCCGTCAGTGACACCATGGCGTCAATTAACCTTGGTGG 398
Qy 61 ValHisSerValPheLeuLeuThrValPropheArgLeuThrThrLeuLeuLysLeuThr 80
Db 399 GTCCACAGCGTTTTCTGCTGACAGTGCCAATTCGCTTGACCTACCTCATCAAGAAGACT 458
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetThr 100
Db 459 TGGATGTTTGGGCTGCCCTTCTGCANAATTTGTGAGTGCCATGCTGCACATCCCATGTAC 518
Qy 101 LeuThrPheLeuPheThrValValIleLeuValThrArgThrLeuLeuPhePheLysCys 120
Db 519 CTCAGTTCCTATTTCTATGTGTGTCATCTGCTGCACAGATACCTCATCTTCTTCAAGTGC 578
Qy 121 LysAspLysValGluPheThrArgLysLeuHisAlaValAlaLysAlaGlyMetThr 140
Db 579 AAAGACAAAGTGAATTTCTACAGAAACCTGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCT 638
Qy 141 ThrLeuValIleValIleValValProLeuValValSerArgThrGlyIleHisGluGlu 160
Db 639 ACGTGGTGTATGTCATTTGGTATCCCTGTTGCTCTCCGGTATGGAATCCATCAGGAA 698
Qy 161 TyrAsnGluHisCysPhePheHisLysGluLeuAlaThrThrThrValLysIle 180
Db 699 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACATATGCCACAGGAG 758
Qy 181 IleAsnThrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 759 ATCACTATATGATGATGTCATTTTGTATAGCCCTTGTGTGATCTTGTGTGCTTCCAG 818
Qy 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 819 GTCCTTCATCATTTATGTTGATGGTGCAGAGCTACGCCACTCTTTTACTATGCCACAGGAG 878
Qy 221 PheThrAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 879 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTCACTCTTGTGTTTCTTCTTCCC 938

```


University, Box 593, Uppsala 75124, Sweden

FEATURES

source

Location/Qualifiers

1..918

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

1..918

/gene="GPR141"

1..918

/gene="GPR141"

/codon_start=1

/product="G protein-coupled receptor 141"

/protein_id="AAP72129.1"

/db_xref="GI:32165524"

/translation="MPGHTSRNSCDPIVTPHLISLYFIVLIGLVGISILFLVK

MNTSRVTMAVINLVVHVSFLITVPRLTIKTMFGLPFCFVSAAMLIHMYLT

FLFYVILVTRYLIFPKCKDVEFYRKLHVAASAGMTLVIIVPLVVSRYGTHEE

YNEHCFFKFLAYTVYKINVMIVFIAVAVILLVQFVFIIMLVQKRLSHLSH

QEFWAQNLNFFIGVILVCLPQYFRIYILNVVTHSNACNSKVAFYNEIFLSVTAIS

CYDLLLFFVGGSHWFQKIIGLWNCVLCR"

ORIGIN

Alignment Scores:

Pred. No.: 1.02e-110 Length: 918
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-055-106C-2 (1-305) x AY288420 (1-918)

Qy 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 1 ATGCCTGGCCACAACTACCTCCAGCAATTCCTTGGCATCCTATAGTGACACCCACTTA 60
Qy 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 61 ATCAGCCTTACTTTCATAGTGCATTATGGCGGCTGGTGGTGCATTTCCATCTCTTC 120
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 60
Db 121 CTCCTGGTGAAGTGAACACCGCTCAGTGACACCACTGGCGGTCACTTAATCTGGTGTG 180
Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
Db 181 GTCCACAGCGTTTTTCTGTCGACAGTGCCATTTCCGCTTGACCTACCTCATCAAGAGACT 240
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 241 TGGATGTTGGGCTGCCCTCTGCAANTTTGTGAGTGCCATGCTGCACATCCCATGTAC 300
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db 301 CTCACGTTCTTATCTATGTTGATCCTGTCACCAAGACTCCTCATCTCTTCTCAAGTGC 360
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetTyr 140
Db 361 AAGACAAAGTGAATTCACAGAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 141 ThrLeuValIleValIleValValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 421 ACGCTGGTATGTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
Qy 161 TyrAsnGluGluHisCysPheLysPheHisGlyLeuLeuAlaTyrThrTyrValLysIle 180
Db 481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTCTTACACATATGTGAATAATC 540
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 541 ATCACTATATGATAGTCATTTTGTGATAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220

Db 601 GTCTTCATCATTAATGTTGAGTGCAGAAAGCTACGCCACTCTTTACTATCCACCAGGAG 660
Qy 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGTCACTCTTGTGTGTTTCTCTCC 720
Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTGTGACGATCCCAATGCCCTGTACAGC 780
Qy 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 781 AAGTTGCAATTTATACGAAATCTTCTTGAGTGTACAGCAATTAGCTGTATGATTG 840
Qy 281 LeuLeuPheValPheGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
Db 841 CTCTCTTTGCTTTTGGGGGAAGCCATGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 900
Qy 301 CysValLeuCysArg 305
Db 901 TGTGTTTGTGCGGT 915

RESULT 6

AX453412
LOCUS AX453412 1051 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 1 from Patent WO244212.
ACCESSION AX453412
VERSION AX453412.1 GI:21712725
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1. Deleersnijder, W., Blockx, H. and de Moor, L.
Human g-protein coupled receptor and uses thereof
Patent: WO 0244212-A 1 06-JUN-2002;
SOLVAY PHARMACEUTICALS B V (NL)

FEATURES

source

1..1051
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
60..977
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD38106.1"
/db_xref="GI:21712726"
/translation="MPGHTSRNSCDPIVTPHLISLYFIVLIGLVGISILFLVK
MNTSRVTMAVINLVVHVSFLITVPRLTIKTMFGLPFCFVSAAMLIHMYLT
FLFYVILVTRYLIFPKCKDVEFYRKLHVAASAGMTLVIIVPLVVSRYGTHEE
YNEHCFFKFLAYTVYKINVMIVFIAVAVILLVQFVFIIMLVQKRLSHLSH
QEFWAQNLNFFIGVILVCLPQYFRIYILNVVTHSNACNSKVAFYNEIFLSVTAIS
CYDLLLFFVGGSHWFQKIIGLWNCVLCR"

CDS

ORIGIN

Alignment Scores:

Pred. No.: 1.17e-110 Length: 1051
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-055-106C-2 (1-305) x AX453412 (1-1051)

Qy 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 60 ATGCCTGGCCACAACTACCTCCAGCAATTCCTTGGCATCCTATAGTGACACCCACTTA 119
Qy 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40

QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260
Db 721 TACAGTCTTTAGGATCTATTAATGATTTGGTGGCCATTCCTATCCCTGTACAGC 780
QY 261 LysValAlaPheTyrAsnGlnPheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 781 AAGGTTGCATTTATTAACGAATCTCTTGTAGGTAAACAGCAATTAGCTGCTATGATTG 840
QY 281 LeuLeuPheValPheGlyGlySerHisTyrPheLeuGlnLysIleLeuLeuTrpAsn 300
Db 841 CTCTCTTTGTCTTTGGGGAGCCATTGGTTTAAAGCAAGATATTGGCTATATGGAAAT 900
QY 301 CysValLeuCysArg 305
Db 901 TGTGTTTGTGCCGT 915
RESULT 4
BD187510
LOCUS
DEFINITION Novel Polypeptide.
ACCESSION BD187510
VERSION BD187510.1 GI:32997249
KEYWORDS JP 2003024082-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Lee H.
TITLE Novel Polypeptide.
JOURNAL Patent: JP 2003024082-A 1 28-JAN-2003;
COMMENT Prizer Limited (EP (GB) only), Pfizer Inc (EP except GB / US / JP)
OS Homo sapiens
PN JP 2003024082-A/1
PD 28-JAN-2003
PF 17-JAN-2002 JP 2002008881
PR 23-JAN-2001 GB 0101739.1
PI harland lee
CC
FH Key Location/Qualifiers.
FEATURES
source
1. 918
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.02e-110 Length: 918
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-055-106C-2 (1-305) x BD187510 (1-918)
QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
Db 1 ATGCTGGCCACATACCTCCAGCAATTCCTTTGGATCCCTATAGTACACCCACTTA 60
QY 21 IleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeuPhe 40
Db 61 ATCAGCCTCTACTTCTATGCTTATTGGCGGCTGGTGGTGCATTTCCTTTTC 120
QY 41 LeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuVal 60
Db 121 CTCTGGTGAATGAAACCCCGGTGAGTACACCCATGGCGGTCAATTAACTTGGTGG 180
QY 61 ValHisSerValPheLeuLeuThrValPropheArgLeuThrTyrLeuIleLysIleThr 80
Db 181 GTCCACAGCGTTTCTGTCAGTGCATTCGCTTACCTTACCTCATCAAGAGACT 240

QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 241 TGGATGTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrIleLeuPhePheLysCys 120
Db 301 CTCAGTTCCTATTCTATGTGGTATCCTGGTCAACAGATACCTCATCTCTTCTTCAAGTGC 360
QY 121 LysAspLysValGluPheTyrAtsGlyLeuHisAlaValAlaIleAsnAlaGlyMetTyr 140
Db 361 AAGACAAAGTGGAAATCTACAGAAACTGCATGCTGTGGTCCAGTGTGGCATGTGG 420
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 421 ACGTGTGTGATTGTCAATGTGGTACCCCTGTTCTCCCGTATGGAATCCATGAGGAA 480
QY 161 TyrAsnGluHisCysPheLysPheHisGlyLeuAlaTyrThrTyrValIle 180
Db 481 TACAAATGAGGAGCACTGTTTAAATTTCAAGAGAGCTTGTACACATATGTGAATTC 540
QY 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 541 ATCAACTATATGATAGTCAATTTTGTGCATAGCCGCTGTGATTCCTGTGGTCTTCCAG 600
QY 201 ValPheIleLeuMetLeuMetValGlnLysLeuArgHisSerLeuSerHisGlnGlu 220
Db 601 GTCTTCATCATATTGTGATGGTGCAGAGCTAGCCACTCTTTTACTATCCACAGGAG 660
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 661 TTTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTGCATCCTTGTGTTCTTCTTCCC 720
QY 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260
Db 721 TACCAGTTCCTTAGGATCTATTACTGAATGTTGTGACGCAATTCCAATGCTGTAAACGC 780
QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280
Db 781 AAGTTGCATTTTATACGAAATCTTCTTGAGTGTACACCAATTAGCTGCTATGATTG 840
QY 281 LeuLeuPheValPheGlyGlySerHisTyrPheLysGlnLysIleGlyLeuTrpAsn 300
Db 841 CTCTCTTTGTCTTTGGGGAGCCATTGGTTTAAAGCAAGATATTGGCTTATGGAAT 900
QY 301 CysValLeuCysArg 305
Db 901 TGTGTTTGTGCCGT 915
RESULT 5
AY288420
LOCUS
DEFINITION Homo sapiens G protein-coupled receptor 141 (GPR141) mRNA, complete cds.
ACCESSION AY288420
VERSION AY288420.1 GI:32165523
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 918)
AUTHORS Fredriksson,R., Hoglund,P.J., Gloriam,D.E., Lagerstrom,M.C. and Schiöth,H.B.
TITLE Seven evolutionarily conserved human rhodopsin G protein-coupled receptors lacking close relatives
JOURNAL FEBS Lett. 554 (3), 381-388 (2003)
MEDLINE 22985413
PubMed 14623098
REFERENCE 2 (bases 1 to 918)
AUTHORS Fredriksson,R., Hoglund,P.J., Gloriam,D.E.I., Lagerstrom,M.C. and Schiöth,H.B.
TITLE Direct Submission
JOURNAL Submitted (30-APR-2003) Neuroscience; Unit of Pharmacology, Uppsala

```

Qy 81 TrpMetPheGlyLeuProPheCysValysPheValSerAlaMetLeuHisMetTyr 100
Db 241 TGGATGTTTGGCTGCCCTTCTGCAATTTTGAGTGCCATGCTGCATCCACATGTAC 300
Qy 101 LeuThrPheLeuPheTyrValValleLeuValThrArgTyrLeuLeuPhePheLysCys 120
Db 301 CTCACGTTCTCTATCTATGTGTGTATCTCTGTCACAGATACCTCATCTTCTCAAGTGC 360
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyr 140
Db 361 AAAGACAAAGTGGAAATCTACAGAAACATGCAATGCTGTGGCTGCCAGTGTGGCATGTGG 420
Qy 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 421 ACGCTGGTGTATGTCATCTGTGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
Db 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTGTGCTACACATATGTGAAATC 540
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 541 ATCACTATATGATGATGATCTATTTGTGATAGCGTGTGCTGTGATCTGTGCTCTCCAG 600
Qy 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 601 GTCTTCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Qy 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 661 TTCGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTGTTGTTGTTGTTGTTGTTGTT 720
Qy 241 TyrGlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
Db 721 TACCAGTCTTTAGGATCTATTTACTTGAATGTTGTGACGCAATTCATGCTGTAAACAGC 780
Qy 261 LysValAlaPheTyrAsnGluLeuPheLeuSerValThrAlaIleSerCysTyrAsnLeu 280
Db 781 AAGGTGTCAATTTATACGAAATCTTCTGTAGTGTACAGCAATGATGCTGTATGATTTG 840
Qy 281 LeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleLeuLeuTrpAsn 300
Db 841 CTCTCTTTGTTCTTTGGGGAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Qy 301 CysValLeuCysArg 305
Db 901 TGTGTTTGTGGCGT 915

RESULT 3
BD105324 918 bp DNA linear PAT 27-AUG-2002
LOCUS Novel G protein-coupled receptor protein and its DNA.
DEFINITION
ACCESSION BD105324
VERSION BD105324.1 GI:22650898
KEYWORDS WO 0196567-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
Moriya.T., Ito.T., Shintani,Y. and Miyajima.N.
Novel G protein-coupled receptor protein and its DNA
Patent: WO 0196567-A 1 20-DEC-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, TAKEO MORIYA, TAKASHI ITO, YASUSHI
SHINTANI, NOBUYUKI MIYAJIMA
OS Homo sapiens (human)
PN WO 0196567-A/1
PD 20-DEC-2001
PF 14-JUN-2001 WO 2001JP005061
PR 15-JUN-2000 JP 00P 184596.19-JUL-2000 JP 00P 223887 PI
TAKEO MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC
C12N15/12, C12N1/21, C07K14/705, C07K16/28, C12P21/02, C12Q1/68, PC
A61K38/00,

```

```

PC A61K45/00, A61K48/00, A61P1/00, A61P3/10, A61P9/00, A61P25/28, PC
A61P29/00,
PC A61P35/00, A61P37/00, G01N33/15, G01N33/50, G01N33/53, G01N33/566//
PC (C12N1/21, C12R1.19), (C12P21/02, C12R1.19)
CC Novel G protein-coupled receptor protein and its DNA FH Key
FT Location/Qualifiers
FT source 1..918
FT /organism="Homo sapiens (human)".
FEATURES
source
Location/Qualifiers
1..918
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1,02e-110 Length: 918
Score: 1522.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-055-106C-2 (1-305) x BD105324 (1-918)
Qy 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 1 ATGCTGCGCACAAATACCTCCAGAAATTCCTCTTGGCATCTTAGTGACACCCCACTTA 60
Qy 21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db 61 ATCAGCCTCTACTTCATGTCCTTATTTGGCGGCTGTGGGTGTCATTTCCATCTCTTTC 120
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 121 CTCCTGTGAAATGAACACCGCTAGTCACCAACCATGGCGGTCACTTAACCTTTGGTGTG 180
Qy 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80
Db 181 GTCCACAGCGTCTTTCGCTGACAGTGCCTATTTGCTTGACCTACCTTCATCAAGAAGACT 240
Qy 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
Db 241 TGGATGTTTGGCTGCCCTTCTGCAATTTTGAGTGCCATGCTGCATGCCATCCACATGTAC 300
Qy 101 LeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCys 120
Db 301 CTCACGTTCTCTATCTATGTGTGTATCTCTGTCACAGATACCTCATCTTCTTCAAGTGC 360
Qy 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyr 140
Db 361 AAAGACAAAGTGGAAATCTACAGAAACATGCAATGCTGTGGCTGCCAGTGTGGCATGTGG 420
Qy 141 ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu 160
Db 421 ACGCTGGTGTATGTCATTTGTGTCACCCCTGTTGCTCCCGTATGGAATCCATGAGGAA 480
Qy 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
Db 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTGTGCTACACATATGTGAAATC 540
Qy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
Db 541 ATCACTATATGATGATGATCTATTTGTGATAGCGTGTGCTGTGATCTGTGCTCTCCAG 600
Qy 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
Db 601 GTCTTCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Qy 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
Db 661 TTCGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTGTTGTTGTTGTTGTTGTTGTT 720

```

AX481576
LOCUS AX481576 918 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 1 from Patent EP1225183.
ACCESSION AX481576
VERSION AX481576.1 GI:22316490
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Harland, L.
TITLE Human g-protein coupled receptor
JOURNAL Patent: EP 1225183-A 1 24-JUL-2002;
Pfizer Limited (GB); PFIZER INC. (US)
FEATURES
source
1..918
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1,02e-110 Length: 918
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-055-106C-2 (1-305) x AX481576 (1-918)
QY 1 MetProGlyHisAsnThrSerArgSerCysAspProIleValThrProHisLeu 20
DB 1 ATGCGTGGCCACCAATACCTCCAGGAATCTCTTGGCATCCTATAGTGACACCCCACTTA 60
QY 21 IleSerLeuTyPheIleValLeuIleGlyValLeuValGlyValIleSerIleLeuPhe 40
DB 61 ATCAGCTCTACTTCTATAGTCTTATTTGGGGGCTGGTGGGTGTCATTTCCTTTC 120
QY 41 LeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
DB 121 CTCCTCGTGAAATGAACACCCCGTCAGTGACCCATCGCGGTCAATTAACCTTGGTGGTG 180
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrlleIleLysIleThr 80
DB 181 GTCCACAGCGTTTCTGCTGACAGTGCCTATTCGCTTACCTCATCAGAGACT 240
QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyrl 100
DB 241 TGGATGTTGGGCTGCCCTTCGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300
QY 101 LeuThrPheLeuPheTyrlleValIleLeuValThrArgTyrlleIlePhePheLysCys 120
DB 301 CTCAGCTTCTATCTATGTTGGTATGCTGGTCAGTACCAGATACCTCATCTTCAAGTGC 360
QY 121 LysAspLysValGluPheTyrlleArgLysLeuHisAlaValAlaSerAlaGlyMetTrp 140
DB 361 AAAGACAAAGTGAATTTACAGAAATTCATGCTGCTGGCTGCCAGTGTGGCATGTGG 420
QY 141 ThrLeuValIleValIleValProLeuValValSerArgTyrlleHisGluGlu 160
DB 421 ACCCTGGTGAATGCTATGTTGGTACCCCTGGTGTCTCCCGGTATGGAATCAATGAGAA 480
QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrlleThrTyrlleVal 180
DB 481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC 540
QY 181 IleAsnTyrlleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200
DB 541 ATCAACTATATGATGATCAATTTTGTGATAGCCGTTGCTGTGATCTGTGGTCTTCCAG 600
QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220

DB 601 GTCTTCATCATTTATGTTGATGGTSCAGAACTACGCCACTCTTTACTATCCCCACAGGAG 660
QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
DB 661 TTCTGGGCTCAGCTGAATAACCTATTTTATAGGGGTGATCCTCTGTTGTTCTTCCC 720
QY 241 TyrGlnPhePheArgIleTyrlleLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
DB 721 TACCAGTCTCTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCTGTAAACAGC 780
QY 261 LysValAlaPheTyrlleGluIlePheLeuSerValThrAlaIleSerCysTyrlleAspLeu 280
DB 781 AAGTTTCATTTATACGAATCTCTTGAGTGTACAGCAATTAGCTGCTATGATTG 840
QY 281 LeuLeuPheValPheGlySerHisTrpPheLysGlnLysIleLeuGlyLeuTrpAsn 300
DB 841 CTCTCTCTTTGCTTTGGGGAAGCCATTGTTTAAAGCAAAAGATAATGGCTTATGGAAT 900
QY 301 CysValLeuCysArg 305
DB 901 TGTGTTTGTGGCGT 915
RESULT 2
AX498180 918 bp DNA linear PAT 26-SEP-2002
LOCUS AX498180
DEFINITION Sequence 3 from Patent WO0242461.
ACCESSION AX498180
VERSION AX498180.1 GI:23343111
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Chen, R., Chu, Z.L., Dang, H.T., Lowitz, K.P. and Pride, C.
TITLE Endogenous and non-endogenous versions of human g protein-coupled receptors
JOURNAL Patents: WO 0242461-A 3 30-MAY-2002;
Arena Pharmaceuticals, Inc. (US)
FEATURES
source
1..918
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1,02e-110 Length: 918
Score: 1592.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-055-106C-2 (1-305) x AX498180 (1-918)
QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
DB 1 ATGCGTGGCCACCAATACCTCCAGGAATCTCTTGGCATCCTATAGTGACACCCCACTTA 60
QY 21 IleSerLeuTyrlleValIleLeuIleGlyValLeuValGlyValIleSerIleLeuPhe 40
DB 61 ATCAGCTTCTACTTCAATAGTCTTATTTGGGGGCTGGTGGGTGTCATTTCCTTTC 120
QY 41 LeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
DB 121 CTCCTCGTGAAATGAACACCCCGTCAGTGACCCATCGCGGTCAATTAACCTTGGTGGTG 180
QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrlleIleLysIleThr 80
DB 181 GTCCACAGCGTTTCTGCTGACAGTGCCTATTCGCTTACCTCATCAGAGACT 240

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 25, 2004, 18:51:16 ; Search time 4425 Seconds
(without alignments)
2987.486 Million cell updates/sec

Title: US-10-055-106C-2
Perfect score: 1592
Sequence: 1 MPGNTRNNSCDPVTPHL.....GGSHWFKQKIIGLWNCVLCR 305

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10055106/runat_21042004_161131_26182/app_query.fasta_1.455
-DB=GenEmbl -QFMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=us10055106@cgn_1_1_3508@runat_21042004_161131_26182 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.fun.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1592	100.0	918	6	AX481576 Sequence
2	1592	100.0	918	6	AX498180 Sequence
3	1592	100.0	918	6	BD105324 Novel G P
4	1592	100.0	918	6	BD187510 Novel Pol
5	1592	100.0	918	9	AY288420 Homo sapi
6	1592	100.0	1051	6	AX453412 Sequence
7	1592	100.0	1336	6	AX709193 Sequence
8	1592	100.0	1340	6	AX709194 Sequence
9	1592	100.0	1460	6	AX709195 Sequence
10	1592	100.0	2525	6	AX147836 Sequence
11	1592	100.0	2525	6	AX521885 Sequence
12	1592	100.0	113306	6	AX646815 Sequence
13	1592	100.0	218188	9	AC083865 Homo sapi
14	1579	99.2	164053	2	AC146385
15	1547	97.2	1499	6	AX451925 Sequence
16	1304	81.9	918	10	AY288427 Mus muscu
17	1304	81.9	206999	10	AC122886 Mus muscu
18	1293	81.2	167316	2	AC078995 Mus muscu
19	1176	73.9	2972	6	AX657538 Sequence
20	1046	65.7	228766	2	AC099132 Rattus no
21	847	53.2	744	10	AY288432 Rattus no
22	787	49.4	456	9	AY255538 Homo sapi
23	750.5	47.1	140539	2	AC079758 Homo sapi
24	674	42.3	447	6	AX147776 Sequence
25	674	42.3	447	6	AX521825 Sequence
26	588.5	37.6	169095	5	EX086685 Zebrafish
27	588.5	37.6	188535	2	EX640462 Danio rer
28	547	34.4	393	10	AY255553 Mus muscu
29	538	33.8	897	6	BD182016 Novel G P
30	423	26.6	140539	2	AC079758 Homo sapi
31	423	26.6	225912	2	AC084210 Homo sapi
32	277	17.4	1146	5	AY241090 Gallus ga
33	252	15.8	1137	5	AY241119 Takifugu
34	249	15.6	137153	5	AL590151 Zebrafish
35	249	15.6	142350	5	EX088596 Zebrafish
36	248	15.6	1430	9	BC035750 Homo sapi
37	247	15.5	1014	6	AX128495 Sequence
38	247	15.5	1014	6	AX549261 Sequence
39	247	15.5	1014	9	AF119711 Homo sapi
40	247	15.5	1014	9	AF133266 Homo sapi
41	247	15.5	1014	9	AY242130 Homo sapi
42	247	15.5	152573	9	AL445202 Human DNA
43	247	15.5	164343	2	AC024593 Homo sapi
44	247	15.5	193302	2	AC021992 Homo sapi
45	246.5	15.5	1020	10	AB052685 Rattus no

ALIGNMENTS

RESULT 1

Cy 105 CATTCCATTCTTTCTCC 124
| | | | | | | | | | | | | | | | | |
Db 34 CATTCCATTCTTTCTCC 53

Search completed: April 25, 2004, 18:51:08
Job time : 2953 secs

QY	362	AAGACAAAGTGGATTTCTACA	382
Db	118	AAGACAAAGTGGATTTCTACA	138
RESULT 14			
AQ488559			
LOCUS		686 bp DNA linear	GSS 24-APR-1999
DEFINITION		RPCI-11-229B2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-229B2,	
ACCESSION		Genomic survey sequence.	
VERSION		AQ488559	
KEYWORDS		GSS.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE		1 (bases 1 to 686)	
AUTHORS		Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.	
TITLE		Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready	
JOURNAL		Map Building	
COMMENT		Unpublished (1997) Other_GSSs: RPCI-11-229B2.TV Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@igr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: SP6 Class: BAC ends. Location/Qualifiers 1..686 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="GDB:758757" /db_xref="taxon:9606" /clone="RPCI-11-229B2" /sex="Male" /cell_type="Lymphocytes" /clone_lib="RPCI-11" /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; RPCI11 Human Male BAC Library"	
FEATURES			
source			
Query Match		2.3%; Score 21; DB 28; Length 686;	
Best Local Similarity		100.0%; Pred.No. 20;	
Matches		21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
ORIGIN			
QY	727	TTCTTTTAGGATCTATTACTTG	747
Db	528	TTCTTTTAGGATCTATTACTTG	548
RESULT 15			
AV309267			
LOCUS		275 bp mRNA linear	EST 11-NOV-1999
DEFINITION		AV309267 RIKEN full-length enriched, 8 days embryo Mus musculus cDNA clone 5730578D17 3', mRNA sequence.	
ACCESSION		AV309267	
VERSION		AV309267.1	
KEYWORDS		GI:6362302	
SOURCE		EST.	
ORGANISM		Mus musculus (house mouse)	
Mus musculus			

KEYWORDS
SOURCE
ORGANISM
 EST.
 Salmo salar (Atlantic salmon)
 Salmo salar
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
REFERENCE
AUTHORS
 1 (bases 1 to 733)
 GRASP Consortium, Davidson, W.S., Koop, B.F. and
 http://web.uvic.ca/cbr/grasp.
TITLE
 A survey of Salmo salar transcripts from high complexity cDNA
 libraries
JOURNAL
COMMENT
 Unpublished (2002)
 Contact: Koop BF
 Centre for Biomedical Research
 University of Victoria
 PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
 Tel: 250 472 4067
 Fax: 250 472 4075
 Email: bkoop@uvic.ca
 Genome Sciences Centre, BC Cancer Agency
 cDNA preparation, sequencing and bioinformatics;
 Y Butterfield, R Kirkpatrick, J Asano, N Gira, R Guin, D Lee,
 S Lee, T Olson, P Pandon, A Prabhu, D Smallus, L Spence, J Stott,
 S Taylor, G Yang, J Schein, S Jones and M Marra.
FEATURES
 source
 1..733
 /organism="Salmo salar"
 /mol_type="mRNA"
 /strain="McConnell"
 /db_xref="taxon:8030"
 /clone_lib="mixed tissue"
 /note="Vector: pCMVSPORT6; Library Creator: Research
 Genetics; Atlantic salmon tissue contributors: Carlo
 Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.),
 Simon Jones (PNS, Nanaimo, B.C.), Seaspring Hatchery
 (Crofton, B.C.), Rachel Roper (University of Victoria)"

Query Match 2.8%; Score 26; DB 13; Length 733;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 652 CACCAGGAGTCTGGGCTCAGCTGAA 677
 |||||
Db 496 CACCAGGAGTCTGGGCTCAGCTGAA 471

RESULT 12
LOCUS
DEFINITION
 CSU-K34.117019.SP6 CSU-K34 Aedes aegypti genomic clone
ACCESSION
 CC093858
VERSION
 CC093858
KEYWORDS
 GSS.
SOURCE
ORGANISM
 Aedes aegypti (yellow fever mosquito)
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes;
 Stegomyia.
REFERENCE
 1 (bases 1 to 501)
AUTHORS
 Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.
TITLE
 End sequencing of Aedes aegypti BACs
JOURNAL
 Unpublished (2003)
COMMENT
 Other-GSSs: CSU-K34.117019.T7
 Contact: Brendan Loftus
 Department of Eukaryotic Genomics
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: entset@gr.org
 Library was provided by Susan Brown and Dennis Knudson at Colorado

State University.
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
source
 1..501
 /organism="Aedes aegypti"
 /mol_type="genomic DNA"
 /db_xref="taxon:7159"
 /clone_lib="CSU-K34.117019"
 /clone_lib="CSU-K34"
 /note="Vector: pBACE3.6; Site 1: EcoRI; Source DNA: Aedes
 aegypti; strain unknown (derived from freshly hatched
 larvae at the Virus Research Centre, Poona, India.
 Reference: SINGH, K. R. P. 1967 Cell cultures derived
 from larvae of Aedes albopictus (Skuse) and Aedes aegypti
 (L.). Current Science 36: 506-508; AIC-10 cell line AICC
 CCL-125"

Query Match 2.4%; Score 22; DB 28; Length 501;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ATACCTCCAGGAATTCCTCTTG 35
 |||||
Db 391 ATACCTCCAGGAATTCCTCTTG 412

RESULT 13
LOCUS
DEFINITION
 T372G04P
 T. brucei sheared genomic DNA clone 372G04, forward sequence,
 genomic survey sequence.
ACCESSION
 AL496132
VERSION
 AL496132.1 GI:11872171
KEYWORDS
 GSS.
SOURCE
 Trypanosoma brucei
ORGANISM
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
REFERENCE
 1 (bases 1 to 338)
AUTHORS
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE
 Direct Submission
JOURNAL
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
COMMENT
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nh@sanger.ac.uk
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/projects/t_brucei/.
Location/Qualifiers
source
 1..338
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="372G04"

Query Match 2.3%; Score 21; DB 29; Length 338;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:3988230"
/tissue_type="spontaneous tumor, metastatic to mammary."
/stem_cell_origin="
/lab_host="DH10B"
/clone_lib="NCI-CCAP Lu29"
/note="Organ: lung; Vector: pCMV-Sport6; Site: 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match          2.8%; Score 27; DB 10; Length 772;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 256 CCCTTCTGCAAAATTTGTGAGTGGCATG 282
      |||||
Db 165 CCCTTCTGCAAAATTTGTGAGTGGCATG 191

RESULT 9
AZ554824
LOCUS          580 bp DNA linear GSS 20-NOV-2000
DEFINITION    RPCI-23-211E13-TV RPCI-23 Mus musculus genomic clone
ACCESSION     RPCI-23-211E13, genomic survey sequence.
VERSION       AZ554824.1 GI:11234644
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 580)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
Akinret, B., Levins, M., McGann, S., Teegaye, G., Geer, K., Krol, M., de
Jong, P., and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-211E13.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igir.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac ends/mouse/bac_end_intro.html
Plate: 211 row: E column: 13
Seq primer: T7
Class: BAC ends.

FEATURES
source          Location/Qualifiers
1..580
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-211E13"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size

```

```

selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "

ORIGIN
Query Match          2.8%; Score 26; DB 28; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 643 TTACTATCCACCAGGAGTTCTGGC 668
      |||||
Db 257 TTACTATCCACCAGGAGTTCTGGC 282

RESULT 10
CB514250/c
LOCUS          648 bp mRNA linear EST 16-MAY-2003
DEFINITION    ssalr9b548309 mixed_tissue Salmo salar cDNA, mRNA sequence.
ACCESSION     CB514250
VERSION       CB514250.1 GI:29325476
KEYWORDS      EST.
SOURCE        Salmo salar (Atlantic salmon)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 648)
GRASP Consortium, Davidson, W.S., Koop, B.F. and
http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA
libraries
Unpublished (2002)
Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020, STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
Genome Sciences Centre, BC Cancer Agency cDNA preparation,
sequencing and bioinformatics: Y Butterfield, R Kirkpatrick, J
Amano, N Ginn, R Guin, D Lee, S Lee, T Olson, P Pandoh, A Prabhu, D
Smalius, L Spence, J Stott, S Taylor, G Yang, J Schein, S Jones and
M Marra.

FEATURES
source          Location/Qualifiers
1..648
/organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"
/db_xref="taxon:8030"
/clone_lib="mixed tissue"
/note="Vector: pCMVSPORT6; Library Creator: Research
Genetics ; Atlantic salmon tissue contributors: Carlo
Blagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.),
Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery
(Crofton, B.C.), Rachel Roper (University of Victoria)"

ORIGIN
Query Match          2.8%; Score 26; DB 14; Length 648;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 652 CACCAGGAGTTCTGGGCTCAGCTGAA 677
      |||||
Db 496 CACCAGGAGTTCTGGGCTCAGCTGAA 471

RESULT 11
CA050323/c
LOCUS          733 bp mRNA linear EST 04-MAR-2003
DEFINITION    ssalr9b520231 mixed_tissue Salmo salar cDNA, mRNA sequence.
ACCESSION     CA050323
VERSION       CA050323.1 GI:24380566

```

```

Best Local Similarity 100.0%; Pred. No. 1.1e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 42; Conservative 0;

QY 38 ATCTATAGTGACACCCCACTTAATCAGCTCTTACTTCATAG 79
Db 143 ATCTATAGTGACACCCCACTTAATCAGCTCTTACTTCATAG 184

RESULT 6
AQ425698/c
LOCUS
DEFINITION
  AQ425698 575 bp DNA linear GSS 24-MAR-1999
  CITBI-E1-2569B12.TF CITBI-E1 Homo sapiens genomic clone 2569B12,
  genomic survey sequence.
ACCESSION
  AQ425698
VERSION
  AQ425698.1 GI:4495786
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 575)
AUTHORS
  Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
  Venter,J.C.
TITLE
  Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
  Map Building
JOURNAL
  Unpublished (1997)
COMMENT
  Other GSSs: CITBI-E1-2569B12.TR
  Contact: Shaying Zhao, William Nierman, Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: hbest@ig.org
  Clones are available from Research Genetics (info@resgen.com). BAC
  end search page:
  http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
  Seq primer: MJ3-21
  Class: BAC ends.
  Location/Qualifiers
    1..575
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /clone="2569B12"
      /sex="male"
      /cell_type="sperm"
      /clone_lib="CITBI-E1"
      /note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
      CalTech Human BAC Library D"

ORIGIN
Query Match 3.2%; Score 29; DB 28; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCTGGCCACATACCTCCAGGAATTC 29
Db 30 ATGCCTGGCCACATACCTCCAGGAATTC 2

RESULT 7.
BG862323
LOCUS
DEFINITION
  BG862323 646 bp mRNA linear EST 29-MAY-2001
  602796201F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917024 5',
  mRNA sequence.
ACCESSION
  BG862323
VERSION
  BG862323.1 GI:14212861
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
  1 (bases 1 to 646)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  JOURNAL
  COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-rc@mail.nih.gov
  Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
  Ph.D.
  CDNA Library Preparation: Life Technologies, Inc.
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LNL at:
  http://image.llnl.gov
  Plate: L1AM10828 row: b column: 01
  High quality sequence stop: 644.
  Location/Qualifiers
    1..646
      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="NMRI"
      /db_xref="taxon:10090"
      /clone="IMAGE:4917024"
      /tissue_type="tumor, gross tissue"
      /dev_stage="5 months"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Mam4"
      /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
      Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
      Library constructed by Life Technologies. Investigators
      providing samples: Lothar Hennighausen/Priscilla Furth,
      NIH Reference for transgenic model: Li et al., Cell Growth
      and Differentiation 7, 3-11 (1996)."

ORIGIN
Query Match 2.9%; Score 27; DB 12; Length 646;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 CCCTTCGCAAAATTTGTGAGTGCCATG 282
Db 562 CCCTTCGCAAAATTTGTGAGTGCCATG 588

RESULT 8
BF160725
LOCUS
DEFINITION
  BF160725 772 bp mRNA linear EST 30-OCT-2000
  601769127F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3988230 5',
  mRNA sequence.
ACCESSION
  BF160725
VERSION
  BF160725.1 GI:11040832
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 772)
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  JOURNAL
  COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-rc@mail.nih.gov
  Tissue Procurement: Gilbert Smith, Ph.D.
  CDNA Library Preparation: Life Technologies, Inc.
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LNL at:
  http://image.llnl.gov
  Plate: L1AM9196 row: f column: 07
  High quality sequence stop: 634.
  Location/Qualifiers
    1..772

```

TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center

Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn

FEATURES

source
1. .499
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 20.6%; Score 189; DB 14; Length 499;
Best Local Similarity 100.0%; Pred. No. 28-89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGSCCAATACCTCCAGGAATTCCTCTTGGCATCCTATAGTGACACCCCACTTA 60
Db 311 ATGCTGSCCAATACCTCCAGGAATTCCTCTTGGCATCCTATAGTGACACCCCACTTA 370
QY 61 ATCAGCCTCTACTTCATAGTCTTATTGGCGGGTGGTGGTGCATTTCCATTTCTTTC 120
Db 371 ATCAGCCTCTACTTCATAGTCTTATTGGCGGGTGGTGGTGCATTTCCATTTCTTTC 430
QY 121 CTCCTGTGAAATGACACCCGCTCAGTGACACCATGGCGGTCATTAAGTGGTG 180
Db 431 CTCCTGTGAAATGACACCCGCTCAGTGACACCATGGCGGTCATTAAGTGGTG 490
QY 181 GTCCACAGC 189
Db 491 GTCCACAGC 499

RESULT 4
BG221739
LOCUS BG221739 283 bp mRNA linear EST 21-APR-2001
DEFINITION RST41554 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG221739
VERSION BG221739.1 GI:13747760
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 283)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression

JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 233.
Location/Qualifiers
1. .283
/organism="Homo sapiens"

FEATURES

source
1. .283
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"

/note="See 'Creation of genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 16.1%; Score 148; DB 12; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGGCCACATACCTCCAGGAATTCCTCTTGGCATCCTATAGTGACACCCCACTTA 60
Db 136 ATGCTGGCCACATACCTCCAGGAATTCCTCTTGGCATCCTATAGTGACACCCCACTTA 195
QY 61 ATCAGCCTCTACTTCATAGTCTTATTGGCGGGTGGTGGTGCATTTCCATTTCTTTC 120
Db 196 ATCAGCCTCTACTTCATAGTCTTATTGGCGGGTGGTGGTGCATTTCCATTTCTTTC 255
QY 121 CTCCTGTGAAATGACACCCGCTCAG 148
Db 256 CTCCTGTGAAATGACACCCGCTCAG 283

RESULT 5
BG461295
LOCUS BG461295 649 bp mRNA linear EST 21-APR-2001
DEFINITION RST44080 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG461295
VERSION BG461295.1 GI:13749801
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 649)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression

JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com.
Location/Qualifiers
1. .649
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

FEATURES

source

ORIGIN

Query Match 4.6%; Score 42; DB 12; Length 649;
1. .649
/organism="Homo sapiens"

end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACe3.6

R.site 1 : EcoRI

R.site 2 : EcoRI

Location/Qualifiers

1. .684

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-007G22.TJ"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RPC1-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 50.4%; Score 463; DB 29; Length 684;
Best Local Similarity 99.8%; Pred. No. 3.8e-236;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 376 TTCTACAGAAACTGATGCTGGCTGCCAGTGTGGCATGTGACGCTGGTGTATGTC 435
DB 25 TTCTACAGAAACTGATGCTGGCTGCCAGTGTGGCATGTGACGCTGGTGTATGTC 84
QY 436 ATTGGTGACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAATACAAATGAGGAGCAC 495
DB 85 ATTGGTGACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAATACAAATGAGGAGCAC 144
QY 496 TGTGTTTAAATTTTCAAAAGAGCTTGTGTACACATATGTGAAATCATCAACTATATGATA 555
DB 145 TGTGTTTAAATTTTCAAAAGAGCTTGTGTACACATATGTGAAATCATCAACTATATGATA 204
QY 556 GTCATTTTGTATACCGTGTGTGATGATCTGTGGTCTTCAGGCTTCATCAATATG 615
DB 205 GTCATTTTGTATACCGTGTGTGATGATCTGTGGTCTTCAGGCTTCATCAATATG 264
QY 616 TTGATGGTGACAGAGCTAGCCACTCTTTACTATCCACAGAGTTCGGCTCAGCTG 675
DB 265 TTGATGGTGACAGAGCTAGCCACTCTTTACTATCCACAGAGTTCGGCTCAGCTG 324
QY 676 AAAAACTATTTTATAGGGTCATCTTGTGTTTCTTCCCTCCACAGTTCCTTTAGG 735
DB 325 AAAAACTATTTTATAGGGTCATCTTGTGTTTCTTCCCTCCACAGTTCCTTTAGG 384
QY 736 ATCTATTACTGATCTGTGACGATTCGATGCTGATGCTGTAACGACAGTTCGATTTAT 795
DB 385 ATCTATTACTGATCTGTGACGATTCGATGCTGATGCTGTAACGACAGTTCGATTTAT 444
QY 796 AACGAAATCTTCTTGAGTGTAAACAGCAATTAGCTGCTATGATTGCTTCTTTGCTTT 855
DB 445 AACGAAATCTTCTTGAGTGTAAACAGCAATTAGCTGCTATGATTGCTTCTTTGCTTT 504
QY 856 GGGGGAAGCCATTGTTTAAAGCAAGATAATTG 889
DB 505 GGGGGAAGCCATTGTTTAAAGCAAGATAATTG 538

```

RESULT 2

AQ888495

LOCUS

DEFINITION

HS_3162_B1_B01_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3162 Col=1 Row=D, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AQ888495.1 GI:6344685
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

1 (bases 1 to 456)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3162 row: D column: 1
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 456.

Location/Qualifiers
1. .456
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3162 Col=1 Row=D"
/sex="male"

/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"

Query Match 26.9%; Score 247; DB 28; Length 456;
Best Local Similarity 99.7%; Pred. No. 1.7e-150;
Matches 297; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 379 TACAGAAAACCTGCATGCTGGCTGCCAGTGTGGCATGTGGAGCTGTGATTCATT 438
DB 1 TACAGAAAACCTGCATGCTGGCTGCCAGTGTGGCATGTGGAGCTGTGATTCATT 60
QY 439 GTGTACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAATACATGAGGACATGT 498
DB 61 GTGTACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAATACATGAGGACATGT 120
QY 499 TTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATCATCAACTATATGATAGTC 558
DB 121 TTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATCATCAACTATATGATAGTC 180
QY 559 ATTTTGTTCATAGCCGTGTGATTCCTGTTGGTCTTCCAGGCTTTCATCATATATGTTG 618
DB 181 ATTTTGTTCATAGCCGTGTGATTCCTGTTGGTCTTCCAGGCTTTCATCATATATGTTG 240
QY 619 ATGTTGCAGAGCTACGCCACTCTTTACTATCCACCAGGAGTTCCTGGGCTCAGCTCA 676
DB 241 ATGTTGCAGAGCTACGCCACTCTTTACTATCCACCAGGAGTTCCTGGGCTCAGCTCA 298

```

ORIGIN
Query Match 26.9%; Score 247; DB 28; Length 456;
Best Local Similarity 99.7%; Pred. No. 1.7e-150;
Matches 297; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 379 TACAGAAAACCTGCATGCTGGCTGCCAGTGTGGCATGTGGAGCTGTGATTCATT 438
DB 1 TACAGAAAACCTGCATGCTGGCTGCCAGTGTGGCATGTGGAGCTGTGATTCATT 60
QY 439 GTGTACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAATACATGAGGACATGT 498
DB 61 GTGTACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAATACATGAGGACATGT 120
QY 499 TTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATCATCAACTATATGATAGTC 558
DB 121 TTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATCATCAACTATATGATAGTC 180
QY 559 ATTTTGTTCATAGCCGTGTGATTCCTGTTGGTCTTCCAGGCTTTCATCATATATGTTG 618
DB 181 ATTTTGTTCATAGCCGTGTGATTCCTGTTGGTCTTCCAGGCTTTCATCATATATGTTG 240
QY 619 ATGTTGCAGAGCTACGCCACTCTTTACTATCCACCAGGAGTTCCTGGGCTCAGCTCA 676
DB 241 ATGTTGCAGAGCTACGCCACTCTTTACTATCCACCAGGAGTTCCTGGGCTCAGCTCA 298

```

RESULT 3
CD699779
LOCUS

DEFINITION

EST161303 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION

CD699779.1 GI:32229387

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 499)

REFERENCE

1 (bases 1 to 499)

Li,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and

Zeng,Y.-X.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 25, 2004, 16:55:20 ; Search time 2948 Seconds
(without alignments)
9299.010 Million cell updates/sec

Title: US-10-055-106C-1
Perfect score: 918
Sequence: 1 atgctgcccacaatacctc.....attgtgtttgtgcgcttag 918

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 12

Total number of hits satisfying chosen parameters: 2158929

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_htc.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_htc.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_mam.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_phg.*
- 27: em_gss_vrl.*
- 28: gb_gss1.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463	50.4	684	29	AG145972 Pan trogl
2	247	26.9	456	28	AQ888495 HS 3162 B
3	189	20.6	499	14	CB699779 EST16303
4	148	16.1	283	12	BG221739 RS741554

5	42	4.6	649	12	BG461295
C	6	2.9	575	28	AQ425698
7	27	2.3	646	12	BG862323
8	27	2.9	772	10	BF160725
9	26	2.8	580	28	AZ554824
C	10	2.8	648	14	CB514250
C	11	2.8	733	13	CA050323
12	22	2.4	501	28	CC093858
13	21	2.3	338	29	TA372604P
14	21	2.3	686	28	AQ488559
15	20	2.2	275	9	AV309267
C	16	2.2	289	29	AL762328
17	20	2.2	347	29	BX652637
18	20	2.2	437	14	CB038895
C	19	2.2	471	13	BY186701
C	20	2.2	491	10	BE292324
C	21	2.2	511	29	CC873862
C	22	2.2	533	28	BZ863698
C	23	2.2	748	28	BZ349419
C	24	2.2	754	13	BU841950
C	25	2.2	753	13	BU562963
C	26	2.2	840	28	CC104935
C	27	2.2	842	13	BU848450
C	28	2.2	928	13	BQ714391
C	29	2.2	934	28	CC122040
C	30	2.2	2417	11	AK077556
C	31	2.2	4331	11	AK037644
C	32	2.2	190	14	CB118082
33	19	2.1	200	13	C03512
34	19	2.1	200	13	BU067021
35	19	2.1	290	13	BU090330
36	19	2.1	298	13	BU890330
C	37	2.1	311	10	BB458215
38	19	2.1	365	9	AU229556
39	19	2.1	366	29	CE641568
C	40	2.1	388	9	AI496614
C	41	2.1	388	10	AM892648
C	42	2.1	391	13	BY291896
C	43	2.1	400	10	BF365191
C	44	2.1	402	12	BI021965
C	45	2.1	415	29	CE255286

ALIGNMENTS

RESULT 1	AG145972	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
LOCUS	AG145972	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
DEFINITION	AG145972	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
ACCESSION	AG145972	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
VERSION	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
KEYWORDS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
SOURCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
ORGANISM	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
REFERENCE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
AUTHORS	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
TITLE	AG145972.1	Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey	684 bp	DNA	linear	GSS 08-JAN-2002
JOURNAL	AG145972.1					

```
* 1 24885: contig of 24885 bp in length
* 24886 24985: gap of unknown length
* 24986 66573: contig of 41588 bp in length
* 66574 66673: gap of unknown length
* 66674 164055: contig of 97382 bp in length.
FEATURES
    source
        1..164055
            /organism="Pan troglodytes"
            /mol_type="genomic DNA"
            /db_xref="taxon:9598"
            /chromosome="UNK"
            /clone="RP43-126C6"
    misc_feature
        1..24885
            /note="assembly_name:Contig3"
    misc_feature
        24986..66573
            /note="assembly_name:Contig4"
    misc_feature
        66674..164055
            /note="assembly_name:Contig5"
ORIGIN
```

```
Query Match      85.7%; Score 787; DB 2; Length 164055;
Best Local Similarity 99.8%; Pred.No. 0;
Matches 887; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTGGCCCAATACCTCCAGAAATTCCTCTTGGCATCCTATAGTGACACCCCACTTA 60
DB 16121 ATGCTGGCCCAATACCTCCAGAAATTCCTCTTGGCATCCTATAGTGACACCCCACTTA 16062

QY 61 ATCAGCCTCTATTCTATAGTGGTTATTTGGGGGGTGGTGGGTGTCATTTCCATCTTTTC 120
DB 16061 ATCAGCCTCTATTCTATAGTGGTTATTTGGGGGGTGGTGGGTGTCATTTCCATCTTTTC 16002

QY 121 CTCCTGGTGAATAAGAACACCGGTCAGTGACCACTGGCGGTCATTAACCTTGGTGGTG 180
DB 16001 CTCCTGGTGAATAAGAACACCGGTCAGTGACCACTGGCGGTCATTAACCTTGGTGGTG 15942

QY 181 GTCCACAGCGTTTCTCTGACAGTGCCATTTGGTTGACCTACCTCATCAAGAGACT 240
DB 15941 GTCCACAGCGTTTCTCTGACAGTGCCATTTGGTTGACCTACCTCATCAAGAGACT 15882

QY 241 TGGATGTTGGGCTGCCCTCTGCAAAATTCGTAGTGCCATGCTGCACATCCACATGTAC 300
DB 15881 TGGATGTTGGGCTGCCCTCTGCAAAATTCGTAGTGCCATGCTGCACATCCACATGTAC 15822

QY 301 CTCAGTTTCTATTCTATGTTGGTGATCTGTGTCACAGATACCTCATCTTCTCAAGTGC 360
DB 15821 CTCAGTTTCTATTCTATGTTGGTGATCTGTGTCACAGATACCTCATCTTCTCAAGTGC 15762

QY 361 AAAGACAAAGTGGAAATCTACAGAAACTGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 420
DB 15761 AAAGACAAAGTGGAAATCTACAGAAACTGCTGCTGGCTGGCTGGCTGGCTGGCTGG 15702

QY 421 ACGCTGGTGATTGTCTATGTTGGTACCCCTGGTGTGTCCTCCGGTATGGAATCCATGAGGAA 480
DB 15701 ACGCTGGTGATTGTCTATGTTGGTACCCCTGGTGTGTCCTCCGGTATGGAATCCATGAGGAA 15642

QY 481 TACAATAGGAGCACTGTTTAAATTCACAAAGAGCTTGCTTACACATATGTGAAAATC 540
DB 15641 TACAATAGGAGCACTGTTTAAATTCACAAAGAGCTTGCTTACACATATGTGAAAATC 15582

QY 541 ATCAACTATATGATAGTCAATTTTGTATAGCCGTGCTGTGATTCGTGGTCTTCCAG 600
DB 15581 ATCAACTATATGATAGTCAATTTTGTATAGCCGTGCTGTGATTCGTGGTCTTCCAG 15522

QY 601 GTCTTCATCATTTATGTTGGTGAGAGCTAGCCACTCTTTACTATCCACAGAG 660
DB 15521 GTCTTCATCATTTATGTTGGTGAGAGCTAGCCACTCTTTACTATCCACAGAG 15462

QY 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTATCCTGTTGTTTCTCTCCC 720
DB 15461 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTATCCTGTTGTTTCTCTCCC 15402

QY 721 TACCAGTTCTTTAGGATCTATTACTTTGAATGTTGTGAGCGCATTCCAATGCTGTAAACAGC 780
```

Search completed: April 25, 2004, 19:56:46

Job time : 3931 secs

```
Db 15401 TACCAGTTCTTTAGGATCTATTACTTTGAATGTTGTGACGCATTCCTATGCTGTAAACAGC 15342
QY 781 AAGGTTGCAATTTTATAACGAAATCTTCTTGGAGTGAACAGCAATTAGCTGCTATGATTTG 840
DB 15341 AAGGTTGCAATTTTATAACGAAATCTTCTTGGAGTGAACAGCAATTAGCTGCTATGATTTG 15282
QY 841 CTTCTCTTTGCTCTTTGGGGGAGCCATTTGGTTTACGAAAGATTAATTG 889
DB 15281 CTTCTCTTTGCTCTTTGGGGGAGCCATTTGGTTTACGAAAGATTAATTG 15233
```


REFERENCE
AUTHORS Deleersnijder W., Blockx, H. and de Moor, I.
TITLE Human g-protein coupled receptor and uses thereof
JOURNAL Patent: WO 0244212-A 1 06-JUN-2002;
SOLWAY PHARMACEUTICALS B V (NL)
FEATURES Location/Qualifiers
source 1..1051
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
CDS 60..977
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD38106.1"
/db_xref="GI:21712726"
/db_xref="REMBL:CAD38106"
/translation="MPGHNTSRSSCDPIVTPHLISLIVFIVLIGLVISILFLVVK
MTRSVTMAVNLVVHVSFLITVFFRLYLIKWTMFGLPFCFKEVSAHLHMYLT
FLFYVILVRLVLEFKDKVFKLHVAASAGMTLVIVIVPLVRSYGIHEE
VNEEHCFKPHKELAVTVKIVINMIVIFVIAVAVILLVQVFIIMLVQKLRHLLSH
QEFWALKNLFTIGVILVCLFVQFRIYLVNVTSHNACNSKVAFYNEIFLSVTAIS
CYDLLLFFVGGSHWFQKILIGLWNCVLCR"

ORIGIN
Query Match 94.4%; Score 867; DB 6; Length 1051;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCTGGGCAATACCTCCAGGAATCTCTTGGCGGCTGGTGGTGCATTTCCATTTCTTTTC 120
DB 60 ATGCTGGGCAATACCTCCAGGAATCTCTTGGCGGCTGGTGGTGCATTTCCATTTCTTTTC 119
QY 61 ATCAGGCTCTACTTATAGTGCCTTATTTGGCGGCTGGTGGTGCATTTCCATTTCTTTTC 120
DB 120 ATCAGGCTCTACTTATAGTGCCTTATTTGGCGGCTGGTGGTGCATTTCCATTTCTTTTC 179
QY 121 CTCTGGTGAATGAACACCGGTGAGTGACACCAATGCGGTGCTTAATTAATCTTGGTGGT 180
DB 180 CTCTGGTGAATGAACACCGGTGAGTGACACCAATGCGGTGCTTAATTAATCTTGGTGGT 239
QY 181 GTCCACAGCTTTTCTGCTGACAGTGCCATTTGCTTGACCTTACCTCAAGAGACT 240
DB 240 GTCCACAGCTTTTCTGCTGACAGTGCCATTTGCTTGACCTTACCTCAAGAGACT 299
QY 241 TGGATGTTGGGTGGCCCTTCTGCAATTTGTGAGTGCCATGCTGACATCCACATGTAC 300
DB 300 TGGATGTTGGGTGGCCCTTCTGCAATTTGTGAGTGCCATGCTGACATCCACATGTAC 359
QY 301 CTCACGTTCTTATCTATGTTGGTGATCTGCTGACAGATACCTCATCTTCTTCAAGTGC 360
DB 360 CTCACGTTCTTATCTATGTTGGTGATCTGCTGACAGATACCTCATCTTCTTCAAGTGC 419
QY 361 AAAGACAAAGTGAATTTCTACAGAAATCTGCTGCTGCCAGTGCCTGAGTGCATGTGG 420
DB 420 AAAGACAAAGTGAATTTCTACAGAAATCTGCTGCTGCCAGTGCCTGAGTGCATGTGG 479
QY 421 ACGTGTGATTTGTCATGTTGTTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480
DB 480 ACGTGTGATTTGTCATGTTGTTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 539
QY 481 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTCTTACACATATGTGAAATC 540
DB 540 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTCTTACACATATGTGAAATC 599
QY 541 ATCAACTATATGATGATCATTTTGTATGACCGTGTGCTGATCTGTTGTTCTTCCAG 600
DB 600 ATCAACTATATGATGATCATTTTGTATGACCGTGTGCTGATCTGTTGTTCTTCCAG 659
QY 601 GTCTTCATCATTTATGTTGATGTTGAGAGTACGCGACCTCTTTACTATATCCACACGAG 660
DB 660 GTCTTCATCATTTATGTTGATGTTGAGAGTACGCGACCTCTTTACTATATCCACACGAG 719
QY 661 TTCTGGGCTCAGCTGAAACCACTATTTTATATAGGGGTGATCCTGTTGTTCTTCCCTCC 720

Db 720 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTGATCCTGTTGTTCTTCCCTCC 779
QY 721 TACAGTCTCTTTAGGATCTATTTAGTGTGTGACGATTCCTCAATGCCTGTACAGC 780
DB 780 TACAGTCTCTTTAGGATCTATTTAGTGTGTGACGATTCCTCAATGCCTGTACAGC 839
QY 781 AAGTTCGCAATTTTATACGAAATCTTCTTGAGTGTACACAGCAATTAGCTGCTATGATTG 840
DB 840 AAGTTCGCAATTTTATACGAAATCTTCTTGAGTGTACACAGCAATTAGCTGCTATGATTG 899
QY 841 CTTCCTCTTTGCTTTTGGGGAAGCCATTTGTTAAGCAAAAGATTAATGCTTATGGAAT 900
DB 900 CTTCCTCTTTGCTTTTGGGGAAGCCATTTGTTAAGCAAAAGATTAATGCTTATGGAAT 959
QY 901 TGTGTTTGTGGCGTTAG 918
DB 960 TGTGTTTGTGGCGTTAG 977

AC146385 164055 bp DNA linear HTG 04-NOV-2003
Pan troglodytes chromosome UNK clone RP43-126C6, *** SEQUENCING IN
PROGRESS ***, 3 unordered pieces.
AC146385
AC146385.2 GI:38154073
HTG, HTGS PHASE1
Pan troglodytes (chimpanzee)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (bases 1 to 164055)
Wilson, R.K.
The sequence of Pan troglodytes clone
2 (bases 1 to 164055)
Wilson, R.K.
Direct Submission
Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 164055)
Wilson, R.K.
Direct Submission
Submitted (04-NOV-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
On Nov 4, 2003 this sequence version replaced gi:33620890.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: C_PT126C06
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 162205 bases at least Q40
Consensus quality: 162489 bases at least Q30
Consensus quality: 162744 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

QY	361	AAAGACAAGTGGGAATTTCTACAGAAAACTGCATGCTGTGGCTGCCAGTGCTGGCATGTGG	420
DB	133483	AAGACAAAAGTGGGAATTTCTACAGAAAACTGCATGCTGTGGCTGCCAGTGCTGGCATGTGG	133542
QY	421	AGCCTGGTGATTGTCATTGTGGTACCCTGGTGTCTCCCGGTATGGAAATCCATGAGGAA	480
DB	133543	AGCCTGGTGATTGTCATTGTGGTACCCTGGTGTCTCCCGGTATGGAAATCCATGAGGAA	133602
QY	481	TACAATGAGGAGCACTGTTTTAAATTTTCAAAAGAGCTTCTTTACACATAATGTGAAAATC	540
DB	133603	TACAATGAGGAGCACTGTTTTAAATTTTCAAAAGAGCTTCTTTACACATAATGTGAAAATC	133662
QY	541	ATCAACTATATGATAGTCATTTTGTGCATAGCCGTTGCTGTGATTCGTTGGTCTTCCAG	600
DB	133663	ATCAACTATATGATAGTCATTTTGTGCATAGCCGTTGCTGTGATTCGTTGGTCTTCCAG	133722
QY	601	GTCCTTCATCATTTATGTTGATGTGCAGAAAGCTAGCCACATCTTTACTATCCCACAGGAG	660
DB	133723	GTCCTTCATCATTTATGTTGATGTGCAGAAAGCTAGCCACATCTTTACTATCCCACAGGAG	133782
QY	661	TTCTGGGCTCACGTGAAAAAAGCTATTTTATAGGGTCACTCTGTTGGTCTTCTTCCC	720
DB	133783	TTCTGGGCTCACGTGAAAAAAGCTATTTTATAGGGTCACTCTGTTGGTCTTCTTCCC	133842
QY	721	TACCAGTCTCTTTAGAGATCTATTACTTTGAATGTGTGACGCATTCCAATGCTGTAAACAG	780
DB	133843	TACCAGTCTCTTTAGAGATCTATTACTTTGAATGTGTGACGCATTCCAATGCTGTAAACAG	133902
QY	781	AGGTTGCAATTTTATAAGCAATCTTCTGATGTGAAGCAATAGCTCTATGATTTG	840
DB	133903	AGGTTGCAATTTTATAAGCAATCTTCTGATGTGAAGCAATAGCTCTATGATTTG	133962
QY	841	CCTCTCTTTGCTCTTTGGGGGAAGCCATTGGTTTAAGCAAAGATAATTTGGCTTATGGAAT	900
DB	133963	CCTCTCTTTGCTCTTTGGGGGAAGCCATTGGTTTAAGCAAAGATAATTTGGCTTATGGAAT	134022
QY	901	TGTTGTTTGTGCGGTAG	918
DB	134023	TGTTGTTTGTGCGGTAG	134040
RESULT	13		
AX451925		1499 bp	DNA linear PAT 03-JUL-2002
LOCUS	AX451925		
DEFINITION	Sequence 22 from Patent WO0226825.		
ACCESSION	AX451925		
VERSION	AX451925.1		
KEYWORDS	GI:21698748		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1		
AUTHORS	Baughn, M.R., Graul, R.C., Walia, N.K., Gandhi, A.R., Hafalia, A.J., Ranumkar, J., Burford, C.M., Thornton, M., Kallik, D.A., Yao, M.G., Elliot, V.S., Burrell, N., Khan, F.A., Yue, H., Lu, Y., Arvizu, C., Roopa, R., Nguyen, D.B., Lee, E.A., Lu, D.A., Ison, C.H., Walsh, R.T. and Pelicky, J.L.		
TITLE	G-protein coupled receptors		
JOURNAL	Patent: WO 0226825-A 22 04-APR-2002;		
FEATURES	Incyte Genomics, Inc. (US) Location/Qualifiers 1..1499 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="Incyte ID No: 6157025CB1"		
ORIGIN			
Query Match	96.6%	Score 887;	DB 6; Length 1499;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches	Conservative	Mismatches 0;	Indels 0 Gaps 0;

Qy		1	ATGCTGGCCACAAATACCTCAGGAATTCCTCTTGGATGCCCTATAGTGACACCCCACCTTA	60
Db		381	ATGCTGGCCACAAATACCTCAGGAATTCCTCTTGGATGCCCTATAGTGACACCCCACCTTA	440
Qy		61	ATCAGCGCTCTACTTCATAGTGTCTTATTTGGCGGCTCGTGGGTGCATTTCCTTCATTTTC	120
Db		441	ATCAGCGCTCTACTTCATAGTGTCTTATTTGGCGGCTCGTGGGTGCATTTCCTTCATTTTC	500
Qy		121	CTCCTGGTGAATAATGAACACC CGGTCA GTGACA CACCATGGCGTCAATTAAC TTGGTGGTG	180
Db		501	CTCCTGGTGAATAATGAACACC CGGTCA GTGACA CACCATGGCGTCAATTAAC TTGGTGGTG	560
Qy		181	GTCACAGCGTTTTCTGTGTGACAGTGCCATTTCGGTTGACCTCACCTCATCAAGAAGACT	240
Db		561	GTCACAGCGTTTTCTGTGTGACAGTGCCATTTCGGTTGACCTCACCTCATCAAGAAGACT	620
Qy		241	TGGATGTTGGGTGCGCTTCGCAAAATTTGTGAGTGCCA TGTGCNATCCACATGTFAC	300
Db		621	TGGATGTTGGGTGCGCTTCGCAAAATTTGTGAGTGCCA TGTGCNATCCACATGTFAC	680
Qy		301	CTCAGGTTCCCTATTCATGTGTGATCTCGGTCA CAGATACCTCATCTTC TTC AAC TGTC	360
Db		681	CTCAGGTTCCCTATTCATGTGTGATCTCGGTCA CAGATACCTCATCTTC TTC AAC TGTC	740
Qy		361	AAAGACAAAGTGAATTTCTACAGAAA CTGCATGCTGTGGCTGCGAGTGTGGCATGTGG	420
Db		741	AAAGACAAAGTGAATTTCTACAGAAA CTGCATGCTGTGGCTGCGAGTGTGGCATGTGG	800
Qy		421	ACGCTGGTGATTTGTCAATTTGGTACCCCTGGTTGTCTCCGGTATGGAATCCATGAGGAA	480
Db		801	ACGCTGGTGATTTGTCAATTTGGTACCCCTGGTTGTCTCCGGTATGGAATCCATGAGGAA	860
Qy		481	TACAAAGAGGAGCACTGTTTTTAAATTTCACAAAGAGCTTGCTTACACATATGTGAAAATC	540
Db		861	TACAAAGAGGAGCACTGTTTTTAAATTTCACAAAGAGCTTGCTTACACATATGTGAAAATC	920
Qy		541	ATCAACTATATGATAGTACATTTTGTTCATAGCCGTTGCTGTGATTCGTGTGGTCTCCAG	600
Db		921	ATCAACTATATGATAGTACATTTTGTTCATAGCCGTTGCTGTGATTCGTGTGGTCTCCAG	980
Qy		601	GTCCTCATCAATTAATTTGATGTTGGTGAGAAGCTAGCCACCTCTTTA CTATCCACAGGAG	660
Db		981	GTCCTCATCAATTAATTTGATGTTGGTGAGAAGCTAGCCACCTCTTTA CTATCCACAGGAG	1040
Qy		661	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGT CATCTCTGTTGTTTCTCTCC	720
Db		1041	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGT CATCTCTGTTGTTTCTCTCC	1100
Qy		721	TACAGTCTTTTAGGATCTATTA CTGAAATGTTGTGACGCAATTC CAATGCTGTAAACAGC	780
Db		1101	TACAGTCTTTTAGGATCTATTA CTGAAATGTTGTGACGCAATTC CAATGCTGTAAACAGC	1160
Qy		781	AAGGTTGCATTTTATTAACGAAATCTTCTGATGTAAACAGCAATTAGCTGCTATGATTG	840
Db		1161	AAGGTTGCATTTTATTAACGAAATCTTCTGATGTAAACAGCAATTAGCTGCTATGATTG	1220
Qy		841	CTTCTCTTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAAT	887
Db		1221	CTTCTCTTTGTCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAAT	1267

RESULT 14
AX453412 LOCUS 1051 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 1 from Patent WO0244212.
ACCESSION AX453412
VERSION AX453412.1 GI:21712725
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

8696	8979	764	755	3414	3439	956	988	4946	4869	14	<800
6	<800	6382	6611	2067	2102	2026	2123	6247	6163	44	<800
663	<800	512	<800	5356	5585	1821	1788	685	<800	10402	10380
122	<800	449	<800	1416	1421	2453	2471	1367	1406	300	<800
174	<800	1059	1063	610	<800	8955	9499	109	<800	5150	5294
4551	4612	70	<800	225	<800	1004	988	3608	3535	3195	3246
952	988	424	<800	932	961	7399	7468	7728	7736	2281	2309
968	988	2594	2670	1982	2102	7516	7468	4264	4301	2740	2804
980	988	3852	3908	29	<800	4119	4107	357	<800	5869	5921
10043	10231	915	918	2663	2719	193	<800	3645	3709	248	<800
2412	2471	5333	5315	5958	5921	2792	2805	1961	2031	3072	3079
3670	3625	4795	4869	448	<800	7034	7468	5668	5588	585	<800
4365	4323	668	<800	8190	8084	4940	4902	957	918	655	<800
27	<800	552	<800	1869	1948	603	<800	5024	4869	1206	1270
9749	10231	1010	1063	3655	3640	761	<800	201	<800	1723	1693
703	<800	884	918	14842	14314	2518	2471	1119	1195	19721	20141
1957	2017	2280	2278	3924	3962	4086	4107	709	<800	2331	2309
2403	2471	4595	4869	591	<800	5916	5835	4907	4869	1940	1993
9	<800	654	<800	1362	1270	6995	6947	1161	1195	5574	5585
359	<800	2624	2670	572	<800	4667	4612	11292	11329	3867	3865
57	<800	13428	13500	2139	2102	10434	10231	6699	6611	1268	1270
2128	2184	12540	12591	1593	1527	1306	1313	1358	1406	8347	8084
1087	1101	4819	4869	2049	2102	374	<800	2400	2394	3636	3640
2839	2805	11280	11329	614	<800	Query Match 100.0%; Score 918; DB 9; Length 218186;					
2787	2805	840	918	7901	8084	Best Local Similarity 100.0%; Pred.No. 0;					
5407	5309	9244	8985	619	<800	Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
3324	3348	1672	1707	5583	5585	1 ATGCGTGGCCACATACCTCCAGGAATTCCTTTGGATCCTATAGTGACACCCACTTA 60					
7246	7468	3195	3163	345	<800	133123 ATGCGTGGCCACATACCTCCAGGAATTCCTTTGGATCCTATAGTGACACCCACTTA 133182					
4508	4455	4273	4301	324	<800	Qy 61 ATCAGCCTCTACTTCATPAGTCTTATTTGGCGGCTGGTGGTGCATTTCCATTTCTTTTC 120					
5815	5686	1980	2031	1496	1421	Db 133183 ATCAGCCTCTACTTCATPAGTCTTATTTGGCGGCTGGTGGTGCATTTCCATTTCTTTTC 133242					
5380	5309	520	<800	6710	6637	Qy 121 CTCCTGTGAAATGACACCCGGTCAGTGACACCACTGCGGTGCTTAACTTGGTGGTG 180					
349	<800	737	755	71	<800	Db 133243 CTCCTGTGAAATGACACCCGGTCAGTGACACCACTGCGGTGCTTAACTTGGTGGTG 133302					
4509	4612	1833	1878	848	877	Qy 181 GTCCACAGCGTTTTCTGTGACAGTGCCATTTGCGTTGACCTTACCTCATCAAGAAGACT 240					
571	<800	8798	8985	6153	6135	Db 133303 GTCCACAGCGTTTTCTGTGACAGTGCCATTTGCGTTGACCTTACCTCATCAAGAAGACT 133362					
4162	4455	2024	2031	4085	4113	Qy 241 TGGATGTTGGGTGGCGCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300					
						Db 133363 TGGATGTTGGGTGGCGCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 133422					
						Qy 301 CTCACGTTCTATTCTATGTTGGTGATCCTGGTCACAGATACCTCATCTTCTTCAAGTGC 360					
						Db 133423 CTCACGTTCTATTCTATGTTGGTGATCCTGGTCACAGATACCTCATCTTCTTCAAGTGC 133482					

```
QY 61 ATCAGCCTTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGGTGTCATTTTCCATCTCTTTTC 120
Db 11600 ATCAGCCTTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGGTGTCATTTTCCATCTCTTTTC 11659
QY 121 CTCCTGGTGAATAACACACCGGTCAGTGACCCACATGGGGTCAATTAATCTTGGTGGT 180
Db 11660 CTCCTGGTGAATAACACACCGGTCAGTGACCCACATGGGGTCAATTAATCTTGGTGGT 11719
QY 181 GTCCACAGGTTTTCTGTGACAGTGCAATTTGCTTGGACCTACCTCATCAAGAAGACT 240
Db 11720 GTCCACAGGTTTTCTGTGACAGTGCAATTTGCTTGGACCTACCTCATCAAGAAGACT 11779
QY 241 TGGATGTTTGGGCTGCCCTCTGCAAAATTTGTAGTGCCATGCTGCACATCCATGATGAC 300
Db 11780 TGGATGTTTGGGCTGCCCTCTGCAAAATTTGTAGTGCCATGCTGCACATCCATGATGAC 11839
QY 301 CTCAGTTCTTATCTATGTGGTGATCTCTGTCACAGATACCTCATCTTCTTCAAGTGC 360
Db 11840 CTCAGTTCTTATCTATGTGGTGATCTCTGTCACAGATACCTCATCTTCTTCAAGTGC 11899
QY 361 AAAGACAAGTGGATCTACAGAAACTGCATGCTGTGGCTGCCAGTGGCATGTGG 420
Db 11900 AAAGACAAGTGGATCTACAGAAACTGCATGCTGTGGCTGCCAGTGGCATGTGG 11959
QY 421 ACGCTGGTGAATGTGATGTCATGTCACCTGCTGTGTCCTCCGGTATGGAATCCATGAGAA 480
Db 11960 ACGCTGGTGAATGTGATGTCATGTCACCTGCTGTGTCCTCCGGTATGGAATCCATGAGAA 12019
QY 481 TACATGAGGAGCATGTTTTAAATTCACAAAGCTGTGTTACACATATGTGAAATC 540
Db 12020 TACATGAGGAGCATGTTTTAAATTCACAAAGCTGTGTTACACATATGTGAAATC 12079
QY 541 ATCAACTATATGATGATCAATTTTGTATAGCCGTTGCTGTGATTCGTGCTTCCAG 600
Db 12080 ATCAACTATATGATGATCAATTTTGTATAGCCGTTGCTGTGATTCGTGCTTCCAG 12139
QY 601 GTCCTTCATCATATGTTGATGGTGAGAGCTAGCCACTCTTTACTATCCACAGAG 660
Db 12140 GTCCTTCATCATATGTTGATGGTGAGAGCTAGCCACTCTTTACTATCCACAGAG 12199
QY 661 TTCTGGGCTCAGCTGAAAAAATCTATTTTATAGGGTCACTCTTTGTTGTTCTTCCC 720
Db 12200 TTCTGGGCTCAGCTGAAAAAATCTATTTTATAGGGTCACTCTTTGTTGTTCTTCCC 12259
QY 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGAGCGCATTCCTGTTGAAAGCTGTAACAGC 780
Db 12360 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGAGCGCATTCCTGTTGAAAGCTGTAACAGC 12319
QY 781 AAGGTGCATTTTATACGAATCTCTTGATGCTAACAGCAATAGCTGCTATGTTG 840
Db 12320 AAGGTGCATTTTATACGAATCTCTTGATGCTAACAGCAATAGCTGCTATGTTG 12379
QY 841 CTTCTCTTTGCTTTGGGGAGCCATTGTTTAAAGCAAAAGATAATTTGGTTATGGAAT 900
Db 12380 CTTCTCTTTGCTTTGGGGAGCCATTGTTTAAAGCAAAAGATAATTTGGTTATGGAAT 12439
QY 901 TGTGTTTGTGCGCTTAG 918
Db 12440 TGTGTTTGTGCGCTTAG 12457
```

```
RESULT 12
AC083865
LOCUS AC083865 218186 bp DNA linear PRI 26-JAN-2001
DEFINITION Homo sapiens chromosome 7 clone RP11-605P22, complete sequence.
ACCESSION AC083865
VERSION AC083865.2 GI:12545315
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE
AUTHORS 1 (bases 1 to 218186)
Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
Olson,M.V.
TITLE Large-scale Mapping and Sequencing of Human Chromosome 7
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 218186)
Kaul,R., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-2000) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 218186)
Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
Olson,M.V.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Jan 26, 2001 this sequence version replaced gi:10567930.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
----- Project Information
Center project name: HsaChr7
Center clone name: RP11-605P22 (djs708)
----- Summary Statistics
Sequencing vector: plasmid; X52328; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 217633 bases at least Q40
Consensus quality: 218145 bases at least Q30
Consensus quality: 218186 bases at least Q20
Insert size: 273875; 19.1% error; agarose-fp
Insert size: 218186; sum-of-contigs
Quality coverage: 8.30x in Q20 bases; agarose-fp
Quality coverage: 10.42x in Q20 bases; sum-of-contigs
-----
Overlapping Sequences:
5': mapping in progress
3': RP11-243B12 (UWGC:djs156) AC018634, 6468-bp overlap
-----
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
-----
This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.
-----
Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.
ECORI HindIII BglII
-----
SeqDerMap FngPrnt SeqDerMap FngPrnt SeqDerMap FngPrnt
```


Db 403 ATCAGGCTCTACTTCATAGTGCTTATTGGCGGCTGGTGGGTGCTCATTTCCATTTCTTTTC 462
Qy 121 CTCCTGGTGAAATGAACCCCGGTGAGTACCAACATGGCGGTGCTAATTAACCTGGTGGT 180
Db 463 CTCCTGGTGAAATGAACCCCGGTGAGTACCAACATGGCGGTGCTAATTAACCTGGTGGT 522
Qy 181 GTCCACAGGTTTTCTGCTGACAGTGCATTTGCTGACCTACTCTCATCAAGAAAGACT 240
Db 523 GTCCACAGGTTTTCTGCTGACAGTGCATTTGCTGACCTACTCTCATCAAGAAAGACT 582
Qy 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCATCCACATGATAC 300
Db 583 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCATCCACATGATAC 642
Qy 301 CTCAGCTTCTTATCTATGCTGATGCTGCTGACAGTACCTCATCTTCTTCAAGTGC 360
Db 643 CTCAGCTTCTTATCTATGCTGATGCTGCTGACAGTACCTCATCTTCTTCAAGTGC 702
Qy 361 AAAGACAAAGTGGAAATCTTACAGAAATGCTGCTGAGTGGTGCAGTGGCGCATGTTG 420
Db 703 AAAGACAAAGTGGAAATCTTACAGAAATGCTGCTGAGTGGTGCAGTGGCGCATGTTG 762
Qy 421 AGCTGGTGAATGCTATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 763 AGCTGGTGAATGCTATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 822
Qy 481 TACAATGAGGAGCACTGTTTTTAAATTTTCAAGAGCTTGTCTTACACATATGTGAAATC 540
Db 823 TACAATGAGGAGCACTGTTTTTAAATTTTCAAGAGCTTGTCTTACACATATGTGAAATC 882
Qy 541 ATCAACTATATGATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 883 ATCAACTATATGATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942
Qy 601 GTCTTTCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 943 GTCTTTCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
Qy 661 TTCTGGGCTCAGTGAAACCTATTTTATAGGGTGCATCTTGTGTTGTTTCTTCTCC 720
Db 1003 TTCTGGGCTCAGTGAAACCTATTTTATAGGGTGCATCTTGTGTTGTTTCTTCTCC 1062
Qy 721 TACCAAGTCTTTAGGATCTATTTACTTGAATGTTGTGAGGCTTCCAAATGCTGTAACAGC 780
Db 1063 TACCAAGTCTTTAGGATCTATTTACTTGAATGTTGTGAGGCTTCCAAATGCTGTAACAGC 1122
Qy 781 AAGTGTGATTTTAAACGAAATCTTCTGAGTGAACAGCAATTAGCTGCTATGATTTG 840
Db 1123 AAGTGTGATTTTAAACGAAATCTTCTGAGTGAACAGCAATTAGCTGCTATGATTTG 1182
Qy 841 CTCTCTTTGCTTTTGGGGAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Db 1183 CTCTCTTTGCTTTTGGGGAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 1242
Qy 901 TGTGTTTTGCGGTAG 918
Db 1243 TGTGTTTTGCGGTAG 1260

RESULT 9
AX147836
LOCUS
DEFINITION
Sequence 81 from Patent WO0136473.
ACCESSION
AX147836
VERSION
AX147836.1 GI:14346839
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Vogeli, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P.,
Slightom, J., Schellin, K.A., Kayes, P.S., Bannigan, C.M., Ruff, V.,

Sejltz, T. and Huff, R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 81 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
Location/Qualifiers
source
1. .2525
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 918; DB 6; Length 2525;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
Db 27 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 86
Qy 61 ATCAGCCTCTACTTTCATAGTCTTATTTGGCGGCTGGTGGGTGCTATTTCCATTTCTTTTC 120
Db 87 ATCAGCCTCTACTTTCATAGTCTTATTTGGCGGCTGGTGGGTGCTATTTCCATTTCTTTTC 146
Qy 121 CTCTGGTGAATGAACACCGGTGAGTACCAACCAATGGCGGTCAATTAACCTTGGTGGTG 180
Db 147 CTCTGGTGAATGAACACCGGTGAGTACCAACCAATGGCGGTCAATTAACCTTGGTGGTG 206
Qy 181 GTCCACAGCGTTTTCTGCTGACAGTGCCTATTTGCTTGCCTTACCTCATCAAGAAAGACT 240
Db 207 GTCCACAGCGTTTTCTGCTGACAGTGCCTATTTGCTTGCCTCATCAAGAAAGACT 266
Qy 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTAC 300
Db 267 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTAC 326
Qy 301 CTCAAGTCTCTATTTATGTTGGTGCCTGCTCAGAGATACCTCATCTTCTTCAAGTGC 360
Db 327 CTCAAGTCTCTATTTATGTTGGTGCCTGCTCAGAGATACCTCATCTTCTTCAAGTGC 386
Qy 361 AAAGACAAAGTGGAAATCTACAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 387 AAAGACAAAGTGGAAATCTACAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 446
Qy 421 ACCTGGTGAATGCTATTTGTTGGTACCCCTGTTGCTCCGGTATGGAATCCATGAGGAA 480
Db 447 ACCTGGTGAATGCTATTTGTTGGTACCCCTGTTGCTCCGGTATGGAATCCATGAGGAA 506
Qy 481 TACAATGAGGAGCACTGTTTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 540
Db 507 TACAATGAGGAGCACTGTTTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 566
Qy 541 ATCAACTATATGATGCTATTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 567 ATCAACTATATGATGCTATTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626
Qy 601 GTCTTTCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 627 GTCTTTCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 686
Qy 661 TTCTGGGCTCAGTGAAACCTATTTTATAGGGGTGCTATCTTGTGTTGTTTCTTCTCC 720
Db 687 TTCTGGGCTCAGTGAAACCTATTTTATAGGGGTGCTATCTTGTGTTGTTTCTTCTCC 746
Qy 721 TACCAGTCTCTTTAGGATCTATTTACTTGAATGTTGTGACGCAATTCCTGCTGTAACAGC 780
Db 747 TACCAGTCTCTTTAGGATCTATTTACTTGAATGTTGTGACGCAATTCCTGCTGTAACAGC 806
Qy 781 AAGTGTGATTTTAAACGAAATCTTCTGAGTGAACAGCAATTAGCTGCTATGATTTG 840
Db 807 AAGTGTGATTTTAAACGAAATCTTCTGAGTGAACAGCAATTAGCTGCTATGATTTG 866
Qy 841 CTCTCTTTGCTTTTGGGGAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900


```
QY 841 CTTCTCTTTGCTTTTGGGGAAGCCATTGGTTTAAGCAAAAGATTAATTTGGCTTATGGAAT 900
Db 1059 CTTCTCTTTGCTTTTGGGGAAGCCATTGGTTTAAGCAAAAGATTAATTTGGCTTATGGAAT 1118
QY 901 TGTGTTTGGCGGTAG 918
Db 1119 TGTGTTTGGCGGTAG 1136

RESULT 7
AX709194 1340 bp DNA linear PAT 04-APR-2003
LOCUS Sequence 53 from Patent WO02063004.
DEFINITION AX709194
ACCESSION AX709194
VERSION AX709194.1 GI:29564788
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baughn,M.R., Tribouley,C.M., Nguyen,D.B., Thornton,M., Yao,M.G.,
Kallik,D.A., Gandhi,A.R., Walla,N.K., Arvizu,C., Elliott,V.S.,
Hafalia,A.J., Ramkumar,J., Pei,J., Tang,Y.T., Yue,H., Reddy,R.,
Burford,N., Lu,D.A., Graul,R.C., Khan,F.A., Walsh,R.T., Ison,C.H.,
Richardson,T.W., Griffin,J.A., Warren,B.A., Yang,J., Lee,E.A. and
Harland,L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 02063004-A 53 15-AUG-2002;
Incyte Genomics, Inc. (US)
FEATURES
Source
1. .1340
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Incyte ID No: 90012586CB1"

ORIGIN
Query Match 100.0%; Score 918; DB 6; Length 1340;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCTGGCCAGATACCTCCAGGAATTCCTTTGGGATCCTATAGTGACCCCACTTA 60
Db 223 ATGCCTGGCCAGATACCTCCAGGAATTCCTTTGGGATCCTATAGTGACCCCACTTA 282
QY 61 ATCAGGCTCTACTTCTATAGTGTATTGGGGCTGGTGGTGTCTATTTCCATCTTTTC 120
Db 283 ATCAGGCTCTACTTCTATAGTGTATTGGGGCTGGTGGTGTCTATTTCCATCTTTTC 342
QY 121 CTCCTGGTGAATAATGAACACCCGGTCAGTGACCAACCATGGCGGTCAATTAACTTGGTGGTG 180
Db 343 CTCCTGGTGAATAATGAACACCCGGTCAGTGACCAACCATGGCGGTCAATTAACTTGGTGGTG 402
QY 181 GTCCACAGGTTTTTCTGCTGACAGTGCCATTTGCTTGACCTTACCTCATCAAGAGACT 240
Db 403 GTCCACAGGTTTTTCTGCTGACAGTGCCATTTGCTTGACCTTACCTCATCAAGAGACT 462
QY 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 300
Db 463 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 522
QY 301 CTCAGCTCTATCTATGTTGGTGTCTGGTGACCAAGATCCTCATCTTCTCAAGTGC 360
Db 523 CTCAGCTCTATCTATGTTGGTGTCTGGTGACCAAGATCCTCATCTTCTCAAGTGC 582
QY 361 AAAGACAAAGTGAATTTCTACAGAAAATGTCATGCTGTGGCTGCCAGTCTGCGCATGTGG 420
Db 583 AAAGACAAAGTGAATTTCTACAGAAAATGTCATGCTGTGGCTGCCAGTCTGCGCATGTGG 642
QY 421 ACCTGGTGAATTTCTATGTTGTTACCCCTGGTGTCTCCCGGTATGGAATTCATGAGGAA 480
Db 643 ACCTGGTGAATTTCTATGTTGTTAGCCCTGGTGTCTCCCGGTATGGAATTCATGAGGAA 702
```

```
QY 481 TACAATGAGGAGCACTGTTTTTAATTTTCAAAAGAGCTTGCCTTACACATATGTGAAATC 540
Db 703 TACAATGAGGAGCACTGTTTTTAATTTTCAAAAGAGCTTGCCTTACACATATGTGAAATC 762
QY 541 ATCAACTATATGATAGTCATTTTGTTCATAGCCGTTGCTGTGATTTCTGTTGGTCTTCCAG 600
Db 763 ATCAACTATATGATAGTCATTTTGTTCATAGCCGTTGCTGTGATTTCTGTTGGTCTTCCAG 822
QY 601 GTCTTCATCATATGTTGATGGTGAGAGCTACGCCACTCTTTTACTATATCCCAACAGGAG 660
Db 823 GTCTTCATCATATGTTGATGGTGAGAGCTACGCCACTCTTTTACTATATCCCAACAGGAG 882
QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCTATCTTGTGTTGTTTCTTCCC 720
Db 883 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCTATCTTGTGTTGTTTCTTCCC 942
QY 721 TACAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAAACAGC 780
Db 943 TACAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAAACAGC 1002
QY 781 AAGTTGCATTTTATACGAATCTTCTTGAGTGTACAGCAATTAGCTCTATGATTG 840
Db 1003 AAGTTGCATTTTATACGAATCTTCTTGAGTGTACAGCAATTAGCTCTATGATTG 1062
QY 841 CTTCTCTTTGCTTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Db 1063 CTTCTCTTTGCTTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 1122
QY 901 TGTGTTTGGCGGTAG 918
Db 1123 TGTGTTTGGCGGTAG 1140

RESULT 8
AX709195 1460 bp DNA linear PAT 04-APR-2003
LOCUS Sequence 54 from Patent WO02063004.
DEFINITION AX709195
ACCESSION AX709195
VERSION AX709195.1 GI:29564789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baughn,M.R., Tribouley,C.M., Nguyen,D.B., Thornton,M., Yao,M.G.,
Kallik,D.A., Gandhi,A.R., Walla,N.K., Arvizu,C., Elliott,V.S.,
Hafalia,A.J., Ramkumar,J., Pei,J., Tang,Y.T., Yue,H., Reddy,R.,
Burford,N., Lu,D.A., Graul,R.C., Khan,F.A., Walsh,R.T., Ison,C.H.,
Richardson,T.W., Griffin,J.A., Warren,B.A., Yang,J., Lee,E.A. and
Harland,L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 02063004-A 54 15-AUG-2002;
Incyte Genomics, Inc. (US)
FEATURES
Location/Qualifiers
1. .1460
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Incyte ID No: 90012670CB1"

ORIGIN
Query Match 100.0%; Score 918; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGGCCCAATACCTCCAGGAATTCCTTTGGGATCCTATAGTGACCCCACTTA 60
Db 343 ATGCTGGCCCAATACCTCCAGGAATTCCTTTGGGATCCTATAGTGACCCCACTTA 402
QY 61 ATCAGCTCTACTTCTATGTTGGTGTCTGGTGACCAAGATCCTCATCTCAAGAGACT 120
Db 343 ATCAGCTCTACTTCTATGTTGGTGTCTGGTGACCAAGATCCTCATCTCAAGAGACT 402
QY 121 CTCCTGGTGAATAATGAACACCCGGTCAGTGACCAACCATGGCGGTCAATTAACTTGGTGGTG 180
Db 343 CTCCTGGTGAATAATGAACACCCGGTCAGTGACCAACCATGGCGGTCAATTAACTTGGTGGTG 402
QY 181 GTCCACAGGTTTTTCTGCTGACAGTGCCATTTGCTTGACCTTACCTCATCAAGAGACT 240
Db 403 GTCCACAGGTTTTTCTGCTGACAGTGCCATTTGCTTGACCTTACCTCATCAAGAGACT 462
QY 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 300
Db 463 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 522
QY 301 CTCAGCTCTATCTATGTTGGTGTCTGGTGACCAAGATCCTCATCTTCTCAAGTGC 360
Db 523 CTCAGCTCTATCTATGTTGGTGTCTGGTGACCAAGATCCTCATCTTCTCAAGTGC 582
QY 361 AAAGACAAAGTGAATTTCTACAGAAAATGTCATGCTGTGGCTGCCAGTCTGCGCATGTGG 420
Db 583 AAAGACAAAGTGAATTTCTACAGAAAATGTCATGCTGTGGCTGCCAGTCTGCGCATGTGG 642
QY 421 ACCTGGTGAATTTCTATGTTGTTACCCCTGGTGTCTCCCGGTATGGAATTCATGAGGAA 480
Db 643 ACCTGGTGAATTTCTATGTTGTTAGCCCTGGTGTCTCCCGGTATGGAATTCATGAGGAA 702
```


121 CTCCTGGTGAATGAAACACCCGGTCAGTGACCAACATGGCGGTCAATTAATCTGGTGGT 180
121 CTCCTGGTGAATGAAACACCCGGTCAGTGACCAACATGGCGGTCAATTAATCTGGTGGT 180
181 GPCACAGGTTTTCTGCTGACAGTGCCATTTGCTGACCTTCACTTCACTCAAGAGACT 240
181 GPCACAGGTTTTCTGCTGACAGTGCCATTTGCTGACCTTCACTTCACTCAAGAGACT 240
241 TGGATGTTGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCAATCCACATGATAC 300
241 TGGATGTTGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCAATCCACATGATAC 300
301 CTCAGGTCCTATTCTATGCTGATGCTGTCACCAATGCTGTCACCAATGCTTCTCAAGTGC 360
301 CTCAGGTCCTATTCTATGCTGATGCTGTCACCAATGCTGTCACCAATGCTTCTCAAGTGC 360
361 AAAGACAAAGTGGAAATTTACAGAAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
361 AAAGACAAAGTGGAAATTTACAGAAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
421 AGCTGGTGAATGTCATTTGCTGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
421 AGCTGGTGAATGTCATTTGCTGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
481 TACAATGAGGACACTGTTTTTAAATTTACAAAGAGCTTGTCTTACACATATGTGAAATC 540
481 TACAATGAGGACACTGTTTTTAAATTTACAAAGAGCTTGTCTTACACATATGTGAAATC 540
541 ATCAACTATATGATGATGATTTTGTGATGAGCGTTGCTGCTGCTGCTGCTGCTGCTGCT 600
541 ATCAACTATATGATGATGATTTTGTGATGAGCGTTGCTGCTGCTGCTGCTGCTGCTGCT 600
601 GTCCTCATCATTTGTTGATGCTGAGAGCTGACGCACTCTTTACTATCCACACAGGAG 660
601 GTCCTCATCATTTGTTGATGCTGAGAGCTGACGCACTCTTTACTATCCACACAGGAG 660
661 TTCTGGGCTCAGTGAAACCTATTTTATAGGGGTGATGCTGCTGCTGCTGCTGCTGCTGCT 720
661 TTCTGGGCTCAGTGAAACCTATTTTATAGGGGTGATGCTGCTGCTGCTGCTGCTGCTGCT 720
721 TACCACTCTTTAGGATCTATTGATGCTGAGCTGCTGAGCTTCCAACTGCTGCTGCTGCTGCT 780
721 TACCACTCTTTAGGATCTATTGATGCTGAGCTGCTGAGCTTCCAACTGCTGCTGCTGCTGCT 780
781 AAGGTTGCAATTTATACCAAAATCTTTTATAGGTTAAGCAATGCTGCTGCTGCTGCTGCT 840
781 AAGGTTGCAATTTATACCAAAATCTTTTATAGGTTAAGCAATGCTGCTGCTGCTGCTGCT 840
841 CTTCTCTTTGCTTTGGGGAGCCATTTGTTTACCAAAAGATTAATGGCTTATGGAAT 900
841 CTTCTCTTTGCTTTGGGGAGCCATTTGTTTACCAAAAGATTAATGGCTTATGGAAT 900
901 TGTGTTTGTGCGGTAG 918
901 TGTGTTTGTGCGGTAG 918

RESULT 6
AX709193
LOCUS AX709193 1336 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 52 from Patent WO02063004.
ACCESSION AX709193
VERSION AX709193.1 GI:29564787
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallik, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S.,
Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,

Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and
Harland, J.
G-protein coupled receptors
Patent: WO 02063004-A 52 15-AUG-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
1. 1336
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Incyte ID No: 90012430CB1"

ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 1336;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 60
DB 219 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 278
QY 61 ATCAGCCTCTACTTCTATAGTGCTTATTTGGCGGCTGCTGGGTGTCATTTCCATTCTTTTC 120
DB 279 ATCAGCCTCTACTTCTATAGTGCTTATTTGGCGGCTGCTGGGTGTCATTTCCATTCTTTTC 338
QY 121 CTCCTGGTGAATGAAACACCCGGTCAGTGACCAACATGGCGGTCAATTAATCTGGTGGT 180
DB 339 CTCCTGGTGAATGAAACACCCGGTCAGTGACCAACATGGCGGTCAATTAATCTGGTGGT 398
QY 181 GTCACAGCCTTTTCTGCTGACAGTGCCATTTGCTGCTGACCTACCTCATCAAGAGACT 240
DB 399 GTCACAGCCTTTTCTGCTGACAGTGCCATTTGCTGCTGACCTACCTCATCAAGAGACT 458
QY 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCAACATCCCATGTAC 300
DB 459 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCAACATCCCATGTAC 518
QY 301 CTCAGTTCCTATTCATGCTGATGCTGCTGACAGATACCTCATCTTCTTCAAGTGC 360
DB 519 CTCAGTTCCTATTCATGCTGATGCTGCTGACAGATACCTCATCTTCTTCAAGTGC 578
QY 361 AAAGACAAAGTGGAAATTTACAGAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 579 AAAGACAAAGTGGAAATTTACAGAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 638
QY 421 ACGTGGTGAATGTCATTTGCTGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 639 ACGTGGTGAATGTCATTTGCTGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698
QY 481 TACAATGAGGACACTGTTTTTAAATTTACAAAGAGCTTGTCTTACACATATGTGAAATC 540
DB 599 TACAATGAGGACACTGTTTTTAAATTTACAAAGAGCTTGTCTTACACATATGTGAAATC 758
QY 541 ATCAACTATATGATGATGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 759 ATCAACTATATGATGATGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
QY 601 GTCCTCATCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 819 GTCCTCATCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
QY 661 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 879 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938
QY 721 TACAATGAGGACACTGTTTTTAAATTTACAAAGAGCTTGTCTTACACATATGTGAAATC 780
DB 939 TACCAGTTCCTTAGGATCTATTACTTGAATGTTGAGCGCATTCCTGCTGCTGCTGCTGCT 998
QY 781 AAGGTTGCAATTTATACCAAAATCTTTTATAGTGTAAACAGCAATGCTGCTGCTGCTGCT 840
DB 999 AAGGTTGCAATTTATACCAAAATCTTTTATAGTGTAAACAGCAATGCTGCTGCTGCTGCT 1058

	Query Match	100.0%;	Score 918;	DB 9;	Length 918;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 918;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
Qy	1	ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGGCATCCTATAGTGCACACCCACTTA	60		
Db	1	ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGGCATCCTATAGTGCACACCCACTTA	60		
Qy	61	ATCAGCCTCTACTTCATAGTGCTATTTGGCGGGCTGTGGTGTGCATTTCCATTTCTTTTC	120		
Db	61	ATCAGCCTCTACTTCATAGTGCTATTTGGCGGGCTGTGGTGTGCATTTCCATTTCTTTTC	120		

Db

601

GTCTTCATCATATGTTGATGGTGAGAGCTACGCCACTCTTTTACTATCCACAGAG

660

Qy

661

TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTATCTTGTGTTTCTTCCC

720

Db

661

TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTATCTTGTGTTTCTTCCC

720

Qy

721

TACAGTCTTTAGATCTATCTTGAATGTTGAGCAGCAATCCAGTCAAGAGC

780

Db

721

TACAGTCTTTAGATCTATCTTGAATGTTGAGCAGCAATCCAGTCAAGAGC

780

Qy

781

AAGGTTGCAATTTTAAACGAATCTTCTTGAGTGTAAACAGCAATTAGCTATGAT

840

Db

781

AAGGTTGCAATTTTAAACGAATCTTCTTGAGTGTAAACAGCAATTAGCTATGAT

840

Qy

841

CTTCTCTTTGCTTTGGGGAGCCATTTGGTTTAAAGCAAGATAATTTGGCTTATG

900

Db

841

CTTCTCTTTGCTTTGGGGAGCCATTTGGTTTAAAGCAAGATAATTTGGCTTATG

900

Qy

901

TGTGTTTGTGCGGTTAG 918

Db

901

TGTGTTTGTGCGGTTAG 918

RESULT 3

BD105324

LOCUS

BD105324

Novel G protein-coupled receptor protein and its DNA.

ACCESSION

BD105324.1

GI:22650898

VERSION

WO 0196567-A/1.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 918)

AUTHORS

Moriya,T., Ito,T., Shintani,Y. and Miyajima,N.

TITLE

Novel G protein-coupled receptor protein and its DNA

JOURNAL

Patent: WO 0196567-A 1 20-DEC-2001;

TAKEDA CHEMICAL INDUSTRIES LTD,TAKEO MORIYA,TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA

COMMENT

OS Homo sapiens (human)

PN WO 0196567-A/1

PD 20-DEC-2001

PF 14-JUN-2001

PR 15-JUN-2000

JP 00P 184596.19-JUL-2000

JP 00P 223887

PI TAKEO MORIYA,TAKASHI ITO, YASUSHI SHINTANI,NOBUYUKI MIYAJIMA

PC C12N15/12,C12N1/21,C07K14/705,C07K16/28,C12P21/02,C12Q1/68,PC A61K38/00,PC A61K45/00,A61K48/00,A61P1/00,A61P3/10,A61P9/00,A61P25/28,PC A61P29/00,PC A61P35/00,A61P37/00,G01N33/15,G01N33/50,G01N33/566//

PC (C12N1/21,C12R1:19),(C12P21/02,C12R1:19)

CC Novel G protein-coupled receptor protein and its DNA

PH Key

FT source

1..918

FT Location/Qualifiers

1..918

Location/Qualifiers

/organism='Homo sapiens (human)'

1..918

/organism='Homo sapiens'

/mol_type='genomic DNA'

/db_xref='taxon:9606'

FEATURES

source

ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 918;

Best Local Similarity 100.0%; Pred. NO. 0;

Mismatches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGGCCACAATACCTCCAGGAATCTCTTGGATCTTATAGTGACACCCACCTTA 60

Db 1 ATGCTGGCCACAATACCTCCAGGAATCTCTTGGATCTTATAGTGACACCCACCTTA 60

Qy 61 ATCAGCTCTACTTCATAGTGTATTATGGCGGCTGGTGGGTGTCATTTCCATTTCTTC 120

Db

61

ATCAGCTCTACTTCATAGTGTATTATGGCGGCTGGTGGGTGTCATTTCCATTTCTTC

120

Qy

121

CTCTCTGGTGAATAAGAACACCCGGTCACTGACCAATCGCGGTCAATTAACCTTGGTGG

180

Db

121

CTCTCTGGTGAATAAGAACACCCGGTCACTGACCAATCGCGGTCAATTAACCTTGGTGG

180

Qy

181

GTCCACAGAGGTTTCTGCTGACAGTCCATTTGCGTTCGCTTACCTCTCATCAAGAGACT

240

Db

181

GTCCACAGAGGTTTCTGCTGACAGTCCATTTGCGTTCGCTTACCTCTCATCAAGAGACT

240

Qy

241

TGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGGCCATGCTGCACATGCTAC

300

Db

241

TGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGGCCATGCTGCACATGCTAC

300

Qy

301

CTCAGCTTCCATTTCTATGTTGGTATCTCTGCTGACAGTCCATCTCATCTTCTTCAAGTGC

360

Db

301

CTCAGCTTCCATTTCTATGTTGGTATCTCTGCTGACAGTCCATCTCATCTTCTTCAAGTGC

360

Qy

361

AAAGACAAAGTGGAAATTTCTACAGAAAACCTGCATGCTGCTGCCAGTGGCATGTTG

420

Db

361

AAAGACAAAGTGGAAATTTCTACAGAAAACCTGCATGCTGCTGCCAGTGGCATGTTG

420

Qy

421

ACGCTGGTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG

480

Db

421

ACGCTGGTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG

480

Qy

481

TACAATGAGAGGACACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTAATAATC

540

Db

481

TACAATGAGAGGACACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTAATAATC

540

Qy

541

ATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

600

Db

541

ATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

600

Qy

601

GTCTTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

660

Db

601

GTCTTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

660

Qy

661

TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTGTTGTTGTTGTTGTTG

720

Db

661

TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTGTTGTTGTTGTTGTTG

720

Qy

721

TACAGTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

780

Db

721

TACAGTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

780

Qy

781

AAGGTTGCAATTTTATACGAATCTTCTTCAAGTGTAAACAGCAATTAGCTCTATGATTTG

840

Db

781

AAGGTTGCAATTTTATACGAATCTTCTTCAAGTGTAAACAGCAATTAGCTCTATGATTTG

840

Qy

841

CTTCTCTTCTTCTTGGGGAGCCATTTGGTTTAAAGCAAGATAATTTGGCTTATGGAAT

900

Db

841

CTTCTCTTCTTCTTGGGGAGCCATTTGGTTTAAAGCAAGATAATTTGGCTTATGGAAT

900

Qy

901

TGTGTTTGTGCGGTTAG 918

Db

901

TGTGTTTGTGCGGTTAG 918

RESULT 4

BD187510

LOCUS

BD187510

Novel Polypeptide.

ACCESSION

BD187510

GI:32997249

VERSION

BD187510.1

GI:32997249

KEYWORDS

JP 2003024082-A/1.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 918)

AUTHORS

Lee,H.

FEATURES Pfizer Limited (GB) ; PFIZER INC. (US)
source Location/Qualifiers
1. .918
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTTTGGGATCCTATAGTACACCCCACTTA 60
Db 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTTTGGGATCCTATAGTACACCCCACTTA 60

QY 61 ATCAGCCTCTACTTCACTAGTCTTATGGGGCTGGTGGTGTCAATTCATTTCTTTTC 120
Db 61 ATCAGCCTCTACTTCACTAGTCTTATGGGGCTGGTGGTGTCAATTCATTTCTTTTC 120

QY 121 CTCTGTGTAATGAACACCCCGTCTAGTACACCAATGCGGTCTTAATCTGGTGGTG 180
Db 121 CTCTGTGTAATGAACACCCCGTCTAGTACACCAATGCGGTCTTAATCTGGTGGTG 180

QY 181 GTCCACAGCGTTTCTGTGACAGTCCCATTTTGGTGGTGTCAATTCATTTCTTTTC 240
Db 181 GTCCACAGCGTTTCTGTGACAGTCCCATTTTGGTGGTGTCAATTCATTTCTTTTC 240

QY 241 TGGATGTTGGGCTGGCTCTTCCAAATTTGTGAGTCCCATTTGCTGGTGGTGGTG 300
Db 241 TGGATGTTGGGCTGGCTCTTCCAAATTTGTGAGTCCCATTTGCTGGTGGTGGTG 300

QY 301 CTCAAGTCTCTATTTCTGTGACAGTCCCATTTTGGTGGTGGTGGTGGTGGTG 360
Db 301 CTCAAGTCTCTATTTCTGTGACAGTCCCATTTTGGTGGTGGTGGTGGTGGTG 360

QY 361 AAAGCAAAAGTGAATTTCTACAGAAATCTGATGCTGGTGGTGGTGGTGGTGGTG 420
Db 361 AAAGCAAAAGTGAATTTCTACAGAAATCTGATGCTGGTGGTGGTGGTGGTGGTG 420

QY 421 ACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 421 ACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480

QY 481 TACAAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGGTACACATATGTGAAATC 540
Db 481 TACAAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGGTACACATATGTGAAATC 540

QY 541 ATCAACTATATGATAGTCACTTTTAAATTTTCAAAAGAGCTTGGTACACATATGTGAAATC 600
Db 541 ATCAACTATATGATAGTCACTTTTAAATTTTCAAAAGAGCTTGGTACACATATGTGAAATC 600

QY 601 GTGTTTGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660

Db 901 TGTGTTTGTGGCTAG 918

RESULT 2
AX498180
LOCUS
DEFINITION
Sequence 3 from Patent WO0242461.
ACCESSION
AX498180
VERSION
AX498180.1 GI:23343111
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Chen, R., Chu, Z.L., Dang, H.T., Lowitz, K.P. and Priddy, C.
Endogenous and non-endogenous versions of human g protein-coupled
receptors
Patent: WO 0242461-A 3 30-MAY-2002;
Arena Pharmaceuticals, Inc. (US)
Location/Qualifiers
1. .918
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTTTGGGATCCTATAGTACACCCCACTTA 60
Db 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTTTGGGATCCTATAGTACACCCCACTTA 60

QY 61 ATCAGCCTCTACTTCACTAGTCTTATGGGGCTGGTGGTGTCAATTCATTTCTTTTC 120
Db 61 ATCAGCCTCTACTTCACTAGTCTTATGGGGCTGGTGGTGTCAATTCATTTCTTTTC 120

QY 121 CTCTGTGTAATGAACACCCCGTCTAGTACACCAATGCGGTCTTAATCTGGTGGTG 180
Db 121 CTCTGTGTAATGAACACCCCGTCTAGTACACCAATGCGGTCTTAATCTGGTGGTG 180

QY 181 GTCCACAGCGTTTCTGTGACAGTCCCATTTTGGTGGTGTCAATTCATTTCTTTTC 240
Db 181 GTCCACAGCGTTTCTGTGACAGTCCCATTTTGGTGGTGTCAATTCATTTCTTTTC 240

QY 241 TGGATGTTGGGCTGGCTCTTCCAAATTTGTGAGTCCCATTTGCTGGTGGTGGTG 300
Db 241 TGGATGTTGGGCTGGCTCTTCCAAATTTGTGAGTCCCATTTGCTGGTGGTGGTG 300

QY 301 CTCAAGTCTCTATTTCTGTGACAGTCCCATTTTGGTGGTGGTGGTGGTGGTG 360
Db 301 CTCAAGTCTCTATTTCTGTGACAGTCCCATTTTGGTGGTGGTGGTGGTGGTG 360

QY 361 AAAGCAAAAGTGAATTTCTACAGAAATCTGATGCTGGTGGTGGTGGTGGTGGTG 420
Db 361 AAAGCAAAAGTGAATTTCTACAGAAATCTGATGCTGGTGGTGGTGGTGGTGGTG 420

QY 421 ACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 421 ACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480

QY 481 TACAAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGGTACACATATGTGAAATC 540
Db 481 TACAAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGGTACACATATGTGAAATC 540

QY 541 ATCAACTATATGATAGTCACTTTTAAATTTTCAAAAGAGCTTGGTACACATATGTGAAATC 600
Db 541 ATCAACTATATGATAGTCACTTTTAAATTTTCAAAAGAGCTTGGTACACATATGTGAAATC 600

QY 601 GTGTTTGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 25, 2004, 17:44:40 ; Search time 3928 Seconds
(without alignments)
10129.558 Million cell updates/sec
Title: US-10-055-106C-1
Perfect score: 918
Sequence: 1 atgcctgccacaatactc.....attgtgtttgtgcgcttag 918
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 12
Total number of hits satisfying chosen parameters: 588639

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: gb_ba.*	GenEmbl.*
2: gb_htg.*	
3: gb_in.*	
4: gb_om.*	
5: gb_ov.*	
6: gb_pat.*	
7: gb_ph.*	
8: gb_pl.*	
9: gb_pr.*	
10: gb_ro.*	
11: gb_sts.*	
12: gb_sy.*	
13: gb_un.*	
14: gb_vi.*	
15: em_ba.*	
16: em_fun.*	
17: em_hum.*	
18: em_in.*	
19: em_mu.*	
20: em_om.*	
21: em_ov.*	
22: em_ph.*	
23: em_pat.*	
24: em_pl.*	
25: em_ro.*	
26: em_sts.*	
27: em_un.*	
28: em_vi.*	
29: em_htg_hum.*	
30: em_htg_inv.*	
31: em_htg_inv.*	
32: em_htg_inv.*	
33: em_htg_mus.*	
34: em_htg_pln.*	
35: em_htg_rod.*	
36: em_htg_mam.*	
37: em_htg_vrt.*	
38: em_sy.*	
39: em_htgo_hum.*	
40: em_htgo_mus.*	
41: em_htgo_other.*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	918	100.0	918	6	AX481576	AX481576 Sequence
2	918	100.0	918	6	AX498180	AX498180 Sequence
3	918	100.0	918	6	BD105324	BD105324 Novel G p
4	918	100.0	918	6	BD187510	BD187510 Novel Pol
5	918	100.0	918	9	AY288420	AY288420 Homo sapi
6	918	100.0	1336	6	AX709193	AX709193 Sequence
7	918	100.0	1340	6	AX709194	AX709194 Sequence
8	918	100.0	1460	6	AX709195	AX709195 Sequence
9	918	100.0	2525	6	AX147836	AX147836 Sequence
10	918	100.0	2525	6	AX521885	AX521885 Sequence
11	918	100.0	113306	6	AX646815	AX646815 Sequence
12	918	100.0	218186	9	AC083865	AC083865 Homo sapi
13	887	96.6	1499	6	AX451925	AX451925 Sequence
14	867	94.4	1051	6	AX453412	AX453412 Sequence
15	787	85.7	164055	2	AC146385	AC146385 Pan trogl
16	690	75.2	972	6	AX57538	AX57538 Sequence
17	456	49.7	456	9	AY255538	AY255538 Homo sapi
18	436	47.5	140539	2	AC079758	AC079758 Homo sapi
19	306	33.3	447	6	AX147776	AX147776 Sequence
20	306	33.3	447	6	AX521825	AX521825 Sequence
21	39	4.2	39	6	AX453425	AX453425 Sequence
22	31	3.4	744	10	AY288432	AY288432 Rattus no
23	31	3.4	228766	2	AC099132	AC099132 Rattus no
24	29	3.2	29	6	AX498203	AX498203 Sequence
25	28	3.1	28	6	AX498202	AX498202 Sequence
26	27	2.9	918	10	AY288427	AY288427 Mus muscu
27	27	2.9	167316	2	AC078995	AC078995 Mus muscu
28	27	2.9	206999	10	AC122886	AC122886 Mus muscu
29	26	2.8	26	6	AX498231	AX498231 Sequence
30	26	2.8	26	6	BD105329	BD105329 Novel G p
31	26	2.8	393	10	AY255553	AY255553 Mus muscu
32	24	2.6	24	6	AX147890	AX147890 Sequence
33	24	2.6	24	6	AX147919	AX147919 Sequence
34	24	2.6	24	6	AX521939	AX521939 Sequence
35	24	2.6	24	6	AX521968	AX521968 Sequence
36	24	2.6	24	6	BD105326	BD105326 Novel G p
37	24	2.6	26	6	AX498200	AX498200 Sequence
38	24	2.6	52	6	AX147891	AX147891 Sequence
39	24	2.6	52	6	AX147920	AX147920 Sequence
40	24	2.6	52	6	AX521940	AX521940 Sequence
41	24	2.6	52	6	AX521969	AX521969 Sequence
42	23	2.5	23	6	AX147892	AX147892 Sequence
43	23	2.5	23	6	AX147921	AX147921 Sequence
44	23	2.5	23	6	AX521941	AX521941 Sequence
45	23	2.5	23	6	AX521970	AX521970 Sequence

ALIGNMENTS

RESULT 1
AX481576
LOCUS
DEFINITION
Sequence 1 from Patent EP1225183.
AX481576
ACCESSION
VERSION
AX481576.1 GI:22316490
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Harland, L.
Human g-protein coupled receptor
Patent: EP 1225183-A 1 24-JUL-2002;
AUTHORS
TITLE
JOURNAL

AX481576 918 bp DNA linear PAT 16-AUG-2002

Mon Apr 26 12:47:10 2004

```

; Patent No. 6046026
; GENERAL INFORMATION:
; APPLICANT: EPLER, CECIL
; APPLICANT: OZENBERGER, BRADLEY
; APPLICANT: HUMES, JEFFREY
; TITLE OF INVENTION: CDNAS ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; FILE REFERENCE: 0646/1A81US1
; CURRENT APPLICATION NUMBER: US/08/676,351C
; CURRENT FILING DATE: 1996-09-12
; EARLIER APPLICATION NUMBER: PCT/US95/00939
; EARLIER FILING DATE: 1995-01-20
; EARLIER APPLICATION NUMBER: US 08/185,360
; EARLIER FILING DATE: 1994-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2706
; TYPE: DNA
; ORGANISM: Rat
; US-08-676-351-1

```

```

Query Match      6.5%; Score 59.8; DB 3; Length 2706;
Best Local Similarity 45.6%; Pred. No. 9e-08;
Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

QY 65 GCCTCTACTTCTATAGTGTATTGGGGGCTGGTGGG---TGTCAATTCCTATCTTTTCC 121
DB 264 GGCTCTACTTGGCTGTGCTCGGGGGCTCTCTGGGGAACGCTCGTCATGTATGTCA 323

QY 122 TCCTGTGTAATGACACCCGCTCAGTCACACCATGGCGGTCAATTAACCTTGGTGGTGG 181
DB 324 TCCTAGGCACACCAAGATGAGACAGCTACCAACATTTACATATTTATCTGGCACATGG 383

QY 182 TCCACAGCGTTTTCTGTGTCAGATGCCATTTGGTTGACCTACCTCATCAAGAAGACTT 241
DB 384 CTGATACCCCTGGTCTTGTCTAACTGCCCTTCAGGGCACAGACATCCTACTGGGCTTCT 443

QY 242 GGATGTTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTACC 301
DB 444 GGCCATTTGGGAATGCACTCTGCAAGACTGTCTATGCTATCGACTACTACAACTGTTTA 503

QY 302 TCACGTTCCCTATTCTATGTGGTGATCCTGGTCACAGATACCTCATCTTTCAAAGTCA 361
DB 504 CCAGCACTTTTACTCTGACCGCATGACGCTAGACCGCTATGTGGCTATCTGCCACCTA 563

QY 362 AAGACAAAGTGGAAATCTCAGAAACTGCTGTGCTGCGCTGCGCTGCGCTGCGCTGCGA 421
DB 564 TCCGTGCCCTTGATGTTCGGACATCCAGCAAGCCAGGCTGTAAATGTGGCCATATGGG 623

QY 422 CGCTGTGATTTGCTATTTGGTACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAAT 481
DB 624 CCTGCTTCAGTGGTGGTGTCTCTGTTGCCATCATGGGTCAGCACAAGTGGAGATG 583

QY 482 ACAATCAGGAGCACTGTTTAAATTTCAAAAGAGCTTCTTACATATGTGAAATCA 541
DB 684 AAGAGATCGAGTGCCTGGTGGAGATCCCTGCCCTCAGGACTATTGGGGCCCTGTATCG 743

QY 542 TCAACTATATGATGATGATTTTGTCTAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
DB 744 CCATCTGCATCTCTCTTTTCTCTCTATCATCCCTGTGTGATCATCTCTGTCTGTACA 803

QY 602 TCTTCATCATTT 612
DB 804 GCCTCATGATT 814

```

Search completed: April 25, 2004, 17:46:11
Job time : 93 secs

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 ORIGINAL SOURCE:
 TISSUE TYPE: Rat brain
 US-08-454-549-1

Query Match 6.5%; Score 59.8; DB 2; Length 2706;
 Best Local Similarity 45.6%; Pred. No. 9e-08;
 Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

```

Qy 65 GCCTCTACTTCATGAGTGTATTTGGGGGCTGGTGGG---TGTCAATTCATTTCTTTCC 121
Db 264 GGCTCTACTTCGCTGTGTCATCGGGGGGCTCTGGGGAACCTGCTCGTCAATGATGCA 323

Qy 122 TCCTGGTGAATGAACACCGGTGAGTGACACACCATGGCGGTCAATTAACCTTGGTGGTGG 181
Db 324 TCCTCAGGACACCAAGATGAAGACAGACTACCAACATTTTACATATTAACTGGCACTGG 383

Qy 182 TCCACAGCGTTTTCGTGTGACAGTGCCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 241
Db 384 CTGATACCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 443

Qy 242 GGATGTTGGCTGCTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 301
Db 444 GGCCATTTGGGAATGCACTCTGCAAGACTGTCTATCGACTACTACAAAGTTTA 503

Qy 302 TCAGGTTCTTCTATGATGCTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
Db 504 CCAGCAGCTTTTACTCTGACCGCTTCCAGGACAGACATCTCTACTGGGCTTCT 563

Qy 362 AAGACAAAGTGAATTTACAGAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421
Db 564 TCCGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 623

Qy 422 CGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 481
Db 624 CCCTGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 683

Qy 482 ACAATGAGGACACTGTTTTAAATTTTCAAAAGAGCTTGTACACATATGTGAAATCA 541
Db 684 AAGAGATCGAGTGCCTGGTGGAGATCCCTGCCCTCAGGACTATGCGGCCCTGATTTCG 743

Qy 542 TCAACTATATGATAGTCATTTTGTGATAGCGGTTGCTGCTGCTGCTGCTGCTGCTGCTG 601
Db 744 CCATCTGATCTTCTCTTTTCTCTCATCCCTGTGCTGATCATCTCTGCTGCTTACA 803

Qy 602 TCTTCATCAT 612
Db 804 GCCTCATGATT 814

```

RESULT 14

US-08-454-552-1
 ; Sequence 1, Application US/08454552
 ; Patent No. 6005072

GENERAL INFORMATION:

APPLICANT: EPPLER, C. Mark
 APPLICANT: OZENERGER, Bradley A.
 APPLICANT: HUMES, Jeffrey D.
 TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby, P.C.
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/454,552
 FILING DATE: 30-MAY-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Robinson, Joseph R.
 REGISTRATION NUMBER: 33,448
 REFERENCE/DOCKET NUMBER: 0646/1A818-US4
 TELEPHONE: (212) 527-7700
 TELEFAX: (212) 753-6237
 TELEX: 236687
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2706 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 ORIGINAL SOURCE:
 TISSUE TYPE: Rat brain
 US-08-454-552-1

Query Match 6.5%; Score 59.8; DB 3; Length 2706;

Best Local Similarity 45.6%; Pred. No. 9e-08;
 Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

```

Qy 65 GCCTCTACTTCATGAGTGTATTTGGGGGCTGGTGGG---TGTCAATTCATTTCTTTCC 121
Db 264 GGCTCTACTTCGCTGTGTCATCGGGGGGCTCTGGGGAACCTGCTCGTCAATGATGCA 323

Qy 122 TCCTGGTGAATGAACACCGGTGAGTGACACACCATGGCGGTCAATTAACCTTGGTGGTGG 181
Db 324 TCCTCAGGACACCAAGATGAAGACAGACTACCAACATTTTACATATTAACTGGCACTGG 383

Qy 182 TCCACAGCGTTTTCGTGTGACAGTGCCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 241
Db 384 CTGATACCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 443

Qy 242 GGATGTTGGCTGCTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 301
Db 444 GGCCATTTGGGAATGCACTCTGCAAGACTGTCTATCGACTACTACAAAGTTTA 503

Qy 302 TCAGGTTCTTCTATGATGCTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
Db 504 CCAGCAGCTTTTACTCTGACCGCTTCCAGGACAGACATCTCTACTGGGCTTCT 563

Qy 362 AAGACAAAGTGAATTTACAGAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421
Db 564 TCCGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 623

Qy 422 CGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 481
Db 624 CCCTGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 683

Qy 482 ACAATGAGGACACTGTTTTAAATTTTCAAAAGAGCTTGTACACATATGTGAAATCA 541
Db 684 AAGAGATCGAGTGCCTGGTGGAGATCCCTGCCCTCAGGACTATGCGGCCCTGATTTCG 743

Qy 542 TCAACTATATGATAGTCATTTTGTGATAGCGGTTGCTGCTGCTGCTGCTGCTGCTGCTG 601
Db 744 CCATCTGATCTTCTCTTTTCTCTCATCCCTGTGCTGATCATCTCTGCTGCTTACA 803

Qy 602 TCTTCATCAT 612
Db 804 GCCTCATGATT 814

```

RESULT 15

US-08-676-351-1
 ; Sequence 1, Application US/08676351C


```
QY 182 TCACAGCGTTTTCTGTCGACAGTGCCATTTTCGCTTGACCTACCTCATCAAGAGACTT 241
Db 450 CTGATACCCCTGGCTTCTGCTAACACTGCCCCCTTCAGGGCAGACATCTACTACTGGGCTTCT 509
QY 242 GGATGTTTGGGCGTCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCGACATCCACATGTACC 301
Db 510 GGCCATTTGGGAATGCACTCTGCAAGACTGTCTATGCTATCGACTACTACAAACATGTTTA 569
QY 302 TCAGTTCCTATTCTATGTTGGTGATCCTGCTCCAGATACCTCATCTCTTCAAGTGCA 361
Db 570 CCAGCACTTTTACTCTGACCGCAGATGAGCGTAGACCGTATGCTGCTACCCCTTA 629
QY 362 AAGACAAAGTGAATTTCTACAGAAAACCTGATGCTGTGGTGGCGATGCTGGCATGTGA 421
Db 630 TCCGTGCCCTTGATGTTGCGACATCCAGCAAGCCAGGCTGTTAATGTGGCCATATGGG 689
QY 422 CGCTGGTGATGTCATTTGTGGTACCCCTGCTGTCTCCCGTATGGAATCCATGAGGAAT 481
Db 690 CCCTGGCTTCACTGCTGGTGGTCTTCTGTCGCAATCATGGTTTCCAGCAAGTGAAGATG 749
QY 482 ACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAATCA 541
Db 750 AAGAGATCGAGTGCTGCTGGTGGAGATCCCTGCCCTCAGGACTATTGGGGCCCTGTATTCG 809
QY 542 TCAACTATATGATAGTCAATTTTGTCTAGCGGTTGCTGTGATTCGTGTTGGTCTTCCAGG 601
Db 810 CCATCTGCATCTCCCTTTTCTCTCATCATCCCTGCTGTGATCATCTCTGTCTGTACTA 869
QY 602 TCTTCATCAAT 612
Db 870 GCCTCATGAT 880

RESULT 12
US-08-986-209A-1
; Sequence 1, Application US/08986209A
; Patent No. 6660496
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Pasternak, Gavril W
; APPLICANT: Pan, Ying-Xian
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING KAPPA OPIOID RECEPTORS, RECEPTORS
; TITLE OF INVENTION: THEREBY, AND USES THEREOF
; FILE REFERENCE: 830002-2004
; CURRENT APPLICATION NUMBER: US/08/986.209A
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 2600
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (299)..(1402)
; OTHER INFORMATION:
US-08-986-209A-1

Query March 6.5%; Score 59.8; DB 4; Length 2600;
Best Local Similarity 44.8%; Pred. No. 8.8e-06;
Matches 272; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

QY 9 CCACAATACCTCCAGGAATTCCTTTGGATGCTCTATAGTGACACCCCACTTAATCAGCCT 68
Db 400 CCTCAATGCTAGCCACAGTGCTTCTGCCCTTGGACTCAAGTCCACCATCGTGGGGCT 459
QY 69 CTACTTCATAGTCTTATTGGGGGCTGGTGG--TGTCATTTCCATTTCTTTCCCTCT 125
Db 460 CTACTTGGCTGTGTCATCGGGGGCTCTCTGGGAAGTCCCTCTGTCATGATGATCATCT 519
QY 126 GGTGAAATGAACACCCCGGTGAGTACACCATGCGGTGCTAATCACTTGGTGGTCA 185
Db 520 CAGGCACACCAAGATGAAGACTGTGTACCAATTTACATATTTAATCTGGCACTGGCTGA 579
```

```
QY 186 CAGCGTTTTCTGTCGACAGTGCCATTTTCGCTTGACCTACCTCATCAAGAGACTTGGAT 245
Db 580 TACCTTGGTCTGCTGACACACTGCCCTTCCAGGGCAGACATCTCTTCTGGGCTTCTGGCC 639
QY 246 GTTGGGCTGGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCGACATCCACATGTACCTCAC 305
Db 640 ATTTGGGAATGCACTGTGCAAGACGGTCAITTGCTATGCTACTACAACTGTTTACCAG 699
QY 306 GTTCTATTCTATGTTGGTGATCCTGTCACCCAGATACCTCATCTTCTCAAGTGCNAAGA 365
Db 700 CACTTTCATTTGACTGCCATGAGTAGACCGTTATGTAGTATCTGCCACCCCTATCCG 759
QY 366 CAAAGTGAATTTCTACAGAAAACCTGATGCTGTGGTGGCAGTGTGCGCATGTGAGCGCT 425
Db 760 TGCCCTTGTATGTTGGACATCCAGTAAAGCCCGAGCGGTTAATGTGGCCATATGGGCCCT 819
QY 426 GGTGATTTGTCATTTGGTGATCCCTGCTGTCTCCCGTATGGAATCCATGAGGAATCAA 485
Db 820 GCTTTCGGTGGTGGTGTCTCTGTTGCCATCATGGGCTCAGCAAGTGGAGGATGAAGA 879
QY 486 TGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAATCATCAA 545
Db 880 GATCGAGTGCCTGGTGGAGATCCCGCCCTCAGGACTATTGGGGCCCTGTATTGGCCAT 939
QY 546 CTATATGATAGTCAATTTTGTCTAGCGGTTGCTGTGATTCGTGTTGGTCTTCCAGGCTT 605
Db 940 CTGCACTCTCTTTTCTCTCATCATCCCGGTTCTGATCATCTCTGCTGCTACAGCT 999
QY 606 CATCAT 612
Db 1000 CATGAT 1006

RESULT 13
US-08-454-549-1
; Sequence 1, Application US/08454549
; Patent No. 5866324
; GENERAL INFORMATION:
; APPLICANT: EPPLER, C. Mark
; APPLICANT: OZENERGER, Bradley A.
; APPLICANT: HUMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454.549
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/1A818-US5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2706 base pairs
; TYPE: nucleic acid
```

Patent No. 6103492
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1273
US-08-889-108-16

Query Match 6.5%; Score 59.8; DB 3; Length 1567;
Best Local Similarity 45.6%; Pred. No. 6.6e-08;
Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;
QY 65 GCCTCTACTTCATAGTCTTATGCGGGCTGGTGGG---TGTCATTTCATTCTTTCC 121
DB 330 GGCTCTACTTGGCTGTGTCATCGGGGGCTCCTGGGAACTGCCCTCATGTATGTCA 389
QY 122 TCCTGGTGAATGAACACCGGTGAGTGCACCATGCGGTCAATTAATTGGTGGTGG 181
DB 330 TCCTCAGGCACACCAAGATGAAGACGTACCAACATTTACATATTTAATCTGGCACTGG 449
QY 182 TCCACAGGGTTTTCTGTGACAGTGCCATTTCGCTTGACCTACCTCATCAAGAAGACTT 241
DB 450 CTGATACCTGGTCTTGCTAACACTGCCCTCCAGGCACACACATCTACTGGGCTTCT 509
QY 242 GGATCTTTGGGCTGCCCTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTACC 301
DB 510 GGCCATTTGGGAATGCATCTGCAAGACTGTCAITGCTACGACTACCAACATGTITTA 569
QY 302 TCACGTTCTATTCATGTGTGATCCTGGTCACCGATACCTCATCTTCTTCAAGTCA 361
DB 570 CCAGCACATTTACTCTGACCGCCCAAGAGGTAGACCGCTATGTGGCTATCTGCCACCTTA 629
QY 362 AAGACAAAGTGAATTTCTACAGAAACTGCATGCTGTGGCTGCCAGTCTGCGCATGTGA 421
DB 630 TCCGTGCCCTTGATCTCGGACATCCAGCAAGCCAGGCTGTTAATGTGGCCATATGGG 689
QY 422 CGCTGGTATTCATTTGTTGGTACCCCTGGTGTGTTCTCCCGGTATGGAATCCATGAGGAAT 481

DB 690 CCCTGGCTTCAGTGGTTGGTGTTCCTGTGCCATCATGGGTTTCAGCACAAAGTGAAGATG 749
QY 482 ACAATGAGGAGCACTGTTTAAATTTACAAAGAGCTTGCCTTACACATATGTGAAATCA 541
DB 750 AAGAGATCAGTCCCTGGTGGAGATCCCTGCCCTCAGACTATTGGGGCCCTGTATTGG 809
QY 542 TCAACTATATGATGATGATCATTTTGTTCATAGCCGTTGCTGTGATCTTGTGGTCTTCCAGG 601
DB 810 CCATCTGCATCTTCCCTTTTCTTTCATCATCCCTGTGCTGATCATCTCTGTCTGTCTACA 869
QY 602 TCTTCATCATTT 512
DB 870 GCCTCATGATT 880
RESULT 11
PCT-US94-10358-16
Sequence 16, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1273
PCT-US94-10358-16

Query Match 6.5%; Score 59.8; DB 5; Length 1567;
Best Local Similarity 45.6%; Pred. No. 6.6e-08;
Matches 251; Conservative 0; Mismatches 297; Indels 3; Gaps 1;
QY 65 GCCTCTACTTCATAGTCTTATGCGGGCTGGTGGG---TGTCATTTCATTCTTTCC 121
DB 330 GGCTCTACTTGGCTGTGTCATCGGGGGCTCCTGGGAACTGCCCTCATGTATGTCA 389
QY 122 TCCTGGTGAATGAACACCGGTGAGTGCACCATGCGGGTCAATTAATTGGTGGTGG 181
DB 390 TCCTCAGGCACCAAGATGAAGACAGCTACCAACATTTACATATTTAATCTGGCACTGG 449

9	CCACAATACCTCCAGGAATTCCTCTTGGCATCCTATAGTGACACCCCACTTAATCAGCCT	68
QY		
262	CCTCAATGCTAGCCACAGTGCCTTCCTGCCCTTGGACTCAAGGTACCATCGTGGGCT	321
Db		
69	CTACTTCATAGTGCTTATTGGGGGCTGGTGG---TGTCAATTTCCATTCTTTTCCCTCCT	125
QY		
322	CTACTTGGCTGTGTGATCGGGGGCTCTGGGGAACTGCCTCGTCATGTATGTCATCCT	381
Db		
126	GGTGAAATGAACACCCGGTCAGTACCAACCATGGCGGTCAATTAACTTGGTGGTGCCA	185
QY		

PRIOR APPLICATION NUMBER: 60/093,002
PRIOR FILING DATE: 1996-07-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 1134
TYPE: DNA
ORGANISM: homo sapiens
US-09-743-871B-14

Query Match 8.0%; Score 73.2; DB 4; Length 1134;
Best Local Similarity 46.8%; Pred. No. 5e-12;
Matches 231; Conservative 0; Mismatches 263; Indels 0; Gaps 0;
QY 118 TTCCTCTGTTGGAATGAACACCCGGTCAGTGACACACATGGCGGTCAATTAACCTGGT 177
Db 223 TGCCTTGTTCATGCACACCAAAATGAAGACAGCCACCAATATTTACATCTTTAACTGGCC 282
QY 178 GTGGTCCACAGGTTTTCTGTGTGACAGTGCCATTTCCGCTTGCACCTACCTCATCAAGAAG 237
Db 293 CTGGCGGACACTCTGTCTGTGTGAGCTGCGCTTCCAGGGCAGGACATCTCTCTGGGC 342
QY 238 ACTTGGATGTTTGGGCTGCTCTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATG 297
Db 343 TTCTGGCGGTTTGGGAATGCGGTGTGCAAGACAGTCATTGCCATTGACTACTACAACATG 402
QY 298 TACCTCAGCTTCTATTCTATGTGTGATCTCTGTGTCACGATACCTCATCTCTTCAAG 357
Db 403 TTCACAGACCTTCACCTTAATCTGCTGATGCTGCTGTCACGATACCTCATCTCTTCAAG 462
QY 358 TGCAAGACAAAGTGGAAATTTACAGAAATTCATGCTGTGCTGCGACAGTGGCGATG 417
Db 463 CCCATCCGTGCGCTCGAGTCCGACGTCAGCAAGGCCAGGCTGTCAATGTGGCCATC 522
QY 418 TGGAGCTGCTGATGTCATGTTGTGTGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 477
Db 523 TGGGCCCTGGCTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
QY 478 GAATACAAATGAGGACACTGTTTTAAATTTCAAGAAAGTGTGCTTACACATATGTGAAA 537
Db 583 GATGAAGAGATCGAGTCCGCTGTGAGATCCCTACCCCTCAGGATTAATGCGGCCGGTG 642
QY 538 ATCATCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
Db 643 TTGCGCATCTGATCTTCT 702
QY 598 CAGGCTTCATCAT 611
Db 703 TACAGCCTCATGAT 716

RESULT 6
US-09-743-871B-13
Sequence 13, Application US/09743871B
Patent No. 6627734
GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICED VARIANTS OF MOUS
FILE OF INVENTION: KAPPA3-RELATED OPIOID RECEPTOR (KOR-3) GENE
FILE REFERENCE: 830002-2001.1
CURRENT APPLICATION NUMBER: US/09/743,871B
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: PCT/US99/15977
PRIOR FILING DATE: 1997-07-15
PRIOR APPLICATION NUMBER: 60/093,002
PRIOR FILING DATE: 1996-07-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 1177
TYPE: DNA
ORGANISM: homo sapiens
US-09-743-871B-13

Query Match 7.6%; Score 70.2; DB 4; Length 1177;
Best Local Similarity 46.6%; Pred. No. 4.1e-11;
Matches 225; Conservative 0; Mismatches 258; Indels 0; Gaps 0;
QY 129 GAAATGAACACCCGGTCAGTGACACACCATGGCGGTCAATTAACCTGGTGGTGGTGGTGGTGGT 188
Db 277 GCACACCAAAATGAAGACAGCCACCAATATTTACATCTTTAACTGGCCCTGGCCGACAC 336
QY 189 CGTTTTCTGTGACAGTGGCCATTTGCTTGAGCTTACCTACCTACATCAAGAGACATGTGATGTT 248
Db 337 TCTGGTCTGTGACGCTGCTGCTTCCAGGGCAGGACATCTCTCTGGGCTTCTGGCCGTT 396
QY 249 TGGGCTGCTTCTGCAAAATTTGTGAGTGCATGCTGTCACATCCACATCTACTACTCAGCTT 308
Db 397 TGGGAATGCTGTGCAAGACAGTCAATGCCATTGACTACTACATCAACATGTTTACCAGCAC 456
QY 309 CCTATTCTATGTGGTGAATCCTGTGTACAGATACCTCATCTCTTCTCAAGTGCAAGACAA 368
Db 457 CTTTACCCCTAACTGACATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 516
QY 369 AGTGGATTTCTACAGAAACTGCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 428
Db 517 CTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 576
QY 429 GATTGTCTATGTGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
Db 577 CTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 636
QY 489 GGAGCT 548
Db 637 CGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 696
QY 549 TATGAT 608
Db 597 CATCT 756
QY 609 CAT 611
Db 757 GAT 759

RESULT 7
US-09-016-434-1417
Sequence 1417, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1417:
SEQUENCE CHARACTERISTICS:
LENGTH: 1973 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9471316
US-09-023-655-1417

208	CTGGGGAACTGCCTTGTGTCATGTACGTCACTCTCAGGCACACCAAAATGAAGACAGCCACC	267
154	ACCATGGCGGTCAATTAACCTGGTGGTGGTCCACAGCGTTTTTCTGTGACAGTGCACATTT	213
268	AATAATTACATCTTTAAACCTGGCCCTGGCCGACACTCTGGTCTGTGACCTGGCCCTTC	327
214	CGCTTGACCTACCTCATCAAGAAGACTTGGATGTTTGGGCTGGCCCTCTGCAAAATTGTG	273
328	CAGGGCAGGACATCCTCTGGGCTTCTGGCCGTTTGGGAATGCGCTGTGCAAGACAGTTC	387
274	AGTGCCCATGCTGCACATCCACATGTACCTCAGTTTCCTATTCTATGTGTGATCCTGTGTC	333
388	ATTGCCAATGTACTACAAACATGTTACCAGGACCTTCACCCCTAACTGGCATGAGTGTG	447
334	ACCAAGATACCTCATCTTCTTCAAGTGCAAAAGACAAAGTGGAACTTCTACAGAAAAC	393
448	GATCGCTATGTAGCCATCTGCCACCCCATCCGTGCCCTCGACGTCGCGACGTCACGAA	507
394	GTGTGGCTGCCAGTGCCTGGCATGTGACGCTGGTGTATGTTCATGTGTGTAACCCCTGGTT	453
508	GCCAGGCTGTCAAATGTGGCCATCTGGGCCCTGGCCCTCTGTGTGCGTGTTCGGTTGCC	567
454	GTCTCCCGGTATGGAAATCCATAGAGAAATACAAATAGGAGACACTGTTTTTAATTTCA	513
568	ATCATGGGCTCGGCAACAGTCCAGGATGAAGAGATCGAGTGCCTGTGGAGATCCCTAC	627
514	GAGCTTGCTTTACACATATGTGAAATCATCAACTATATGATAGTCACTTTTGTTCATAG	573
628	CCTCAGGATTACTGGGGCCGGTGTGTGGCAATCTGCATCTTCCCTCTCTCTCTCATCGTC	687
574	GTGTGTGATTCCTGTGGTCTTCAGGCTCTTCATCAT	611
688	CCCGTCTCGTCACTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	725

RESULT 2

US-09-016-434-1391
; Sequence 1391 Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1391:

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/823,114
FILING DATE: 29-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/148,351
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1805 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 10..1119
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-823-114-18

Query Match 8.3%; Score 76.4; DB 9; Length 1805;
Best Local Similarity 46.7%; Pred. No. 4,6e-12;
Matches 242; Conservative 0; Mismatches 276; Indels 0; Gaps 0;
Qy 94 CTGGTGGGTGTCAATTCATCTTTTCTCTCTGGTGAATAAGAACCCCGGTCAAGTACC 153
Db 208 CTGGGAACCTGCTGTGTCATGTACGTCTCTCAGGCACACCAAAATGAAGACAGCCACC 267
Qy 154 ACCATGGCGGTCAATTAATCTGGTGGTGGTCCACAGCGTTTCTCTGTGACAGTGGCAATTT 213
Db 268 AATATTACATCTTTAACTGGCCCTGGCCGACACTCTGGTCTCTGCTGAGCGTCCCTTC 327
Qy 214 CGCTTGACCTACCTCATCAAGAAGACTTGGATGTTGGGCTGCCCTTCTGCAAAATTTGTG 273
Db 328 CAGGCGACGGACATCTCTCTGGCTTCTGGCGTTTGGGAATGCGTGTGCAAGACAGTC 387
Qy 274 AGTGCATGCTGCACATCCATGATCTACCTGCTACGTTCTCTATCTATGTGGTGATCTGTC 333
Db 388 ATTGCCATTGACTACTACCAATGTTTACACAGCACCTTCACTCCCTAACTGCCATGAGTGTG 447
Qy 334 ACCAGATACCTCATCTTCTTCAAGTGCAAGACAAAGTGAATTTCTACAGAAAACCTGCAT 393
Db 448 GATCGTATGTAGCATCTGCCACCCATCGCTGCCCTCGACGTCGCGACGTCAGCAAA 507
Qy 394 GCTGTGGCTGCAGTCTGGGATGTGGACGCTGGTGTGATGATTCATGTGGTACCCCTGTT 453
Db 508 GCCCAGGCTGTCAATGTGGCCATCTGGGCCCTGGCCCTGTGTGCGGTGTTCCCGTTGCC 567
Qy 454 GTCTCCCGGTATGGAATCCATGAGGAATACAAATGAGGAGCACTGTTTAAATTTCAAAA 513
Db 568 ATCATGGCTCGGCACAGGTGAGGATGAAGATGAGTGCCTGGTGGAGATCCCTACC 627
Qy 514 GAGCTTGCTTACACATATGTGAAATAATCATCAACTATATGATGATGATTTTGTGATAGCC 573

Db 628 CCTCAGATTACTGGGGCCCGGTGTTTGGCACTGTGCATCTTCTCTCTCTCAATGTC 687
Qy 574 GTTGTGTGATTTCTGTGTGTCTTCCAGGTCTTTCATCAT 611
Db 688 CCGGTGCTCGTCATCTCTGTCTGTCTACAGCCTCATGAT 725

Search completed: April 25, 2004, 17:54:03
Job time : 462 Secs


```
Db 12260 TACGAGTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCCTCAATGCCGTGTACAGC 12319
Qy 781 AAGTTGCAATTTTATAACGAATCTTCTTGAGTGTAAACAGCAATTAAGCTGTGCTATGATTTG 840
Db 12320 AAGTTGCAATTTTATAACGAATCTTCTTGAGTGTAAACAGCAATTAAGCTGTGCTATGATTTG 12379
Qy 841 CTTCTCTTTTGTCTTTTGGGGGAAGCCATTTGTTTAAAGCAAAAGATTAATTCGCTTATGGAAAT 900
Db 12380 CTTCTCTTTTGTCTTTTGGGGGAAGCCATTTGTTTAAAGCAAAAGATTAATTCGCTTATGGAAAT 12439
Qy 901 TGTGTTTTGTGCCGTTAG 918
Db 12440 TGTGTTTTGTGCCGTTAG 12457

RESULT 10
US-10-085-233B-1
; Sequence 1, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
; FILE REFERENCES: MPI2001-021P1RCP1M
; CURRENT APPLICATION NUMBER: US/10/085,233B
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/272,677
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (147)...(1085)
; OTHER INFORMATION: n at position 1384 can be any
; OTHER INFORMATION: nucleotide
US-10-085-233B-1

Query Match 99.8%; Score 916.4; DB 15; Length 1684;
Best Local Similarity 99.9%; Pred. No. 1.3e-269;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCCTGGCCACATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 60
Db 171 ATGCCTGGCCACATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 230
Qy 61 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGGTGCTATTTCCCATTTCTTTTC 120
Db 231 ATCAGCCTCTACTTCATAGTGTCTTATGGCGGCTGGTGGGTGCTATTTCCCATTTCTTTTC 290
Qy 121 CTCCTGGTGAATAATGAACACCCGGTCAGTGACACCAATGGCGGTCAATTAACCTTGTGGTG 180
Db 291 CTCCTGGTGAATAATGAACACCCGGTCAGTGACACCAATGGCGGTCAATTAACCTTGTGGTG 350
Qy 181 GTCCACAGCGTTTTCTCTGTGACAGTGCCATTTCCGCTTACCTCATCAAGAAGACT 240
Db 351 GTCCACAGCGTTTTCTCTGTGACAGTGCCATTTCCGCTTACCTCATCAAGAAGACT 410
Qy 241 TGGATTTTGGGTGCGCTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
Db 411 TGGATTTTGGGTGCGCTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 470
Qy 301 CTCACGTTCCCTATTTCTATGTTGATCTGCTGATCCAGATACCTCATCTTCTCAAGTGC 360
Db 471 CTCACGTTCCCTATTTCTATGTTGATCTGCTGATCCAGATACCTCATCTTCTCAAGTGC 530
Qy 361 AAAGCAAAAGTGAATTTCTACAGAAACTGCATGTGTGGCTGCCAGTCTGGCATGTGG 420
Db 531 AAAGCAAAAGTGAATTTCTACAGAAACTGCATGTGTGGCTGCCAGTCTGGCATGTGG 590
```

```
Qy 421 ACGCTGGTGATTTGTCATTTGGTACCCCTGGTTGTTCTCCCGGTATGGAATCCCATGAGAA 480
Db 591 ACGCTGGTGATTTGTCATTTGGTACCCCTGGTTGTTCTCCCGGTATGGAATCCCATGAGAA 650
Qy 481 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 540
Db 651 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 710
Qy 541 ATCAACTATATGATAGTCAATTTTGTTCATAGCCGTTGCTGTGATCTCTGTTGGTCTTCCAG 600
Db 711 ATCAACTATATGATAGTCAATTTTGTTCATAGCCGTTGCTGTGATCTCTGTTGGTCTTCCAG 770
Qy 601 GTCCTTCATCATTTATGTTGATGTCAGAGCTAGCCCACTCTTTACTATATCCACAGGAG 660
Db 771 GTCCTTCATCATTTATGTTGATGTCAGAGCTAGCCCACTCTTTACTATATCCACAGGAG 830
Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCCCTCC 720
Db 831 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCCCTCC 890
Qy 721 TACCAGTCTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCGAATGCTGTAAACAGC 780
Db 891 TACCAGTCTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCGAATGCTGTAGCAGC 950
Qy 781 AAGTTGCAATTTTATAACGAATCTTCTTGGTGTAAACAGCAATTAAGCTGTATGATTG 840
Db 951 AAGTTGCAATTTTATAACGAATCTTCTTGGTGTAAACAGCAATTAAGCTGTATGATTG 1010
Qy 841 CTTCTCTTTGCTTTTGGGGGAAGCCATTTGTTTAAAGCAAAAGATTAATTCGCTTATGGAAT 900
Db 1011 CTTCTCTTTGCTTTTGGGGGAAGCCATTTGTTTAAAGCAAAAGATTAATTCGCTTATGGAAT 1070
Qy 901 TGTGTTTTGTGCCGTTAG 918
Db 1071 TGTGTTTTGTGCCGTTAG 1088

RESULT 11
US-10-085-233B-3
; Sequence 3, Application US/10085233B
; Publication No. US20030087249A1
; GENERAL INFORMATION:
; APPLICANT: GLUCKSMANN, MARIA ALEXANDRA
; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
; FILE REFERENCES: MPI2001-021P1RCP1M
; CURRENT APPLICATION NUMBER: US/10/085,233B
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/272,677
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(939)
US-10-085-233B-3

Query Match 99.5%; Score 913.4; DB 15; Length 939;
Best Local Similarity 99.9%; Pred. No. 7.2e-269;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCCTGGCCACATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 60
Db 25 ATGCCTGGCCACATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 84
Qy 61 ATCAGCCTCTACTTCATAGTGTCTTATTTGGCGGCTGGTGGGTGTCAATTTCCATTTCTTTTC 120
Db 85 ATCAGCCTCTACTTCATAGTGTCTTATTTGGCGGCTGGTGGGTGTCAATTTCCATTTCTTTTC 144
```

Db 267 TGGATGTTTGGCTGCGCTCTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 326
Qy 301 CTCAGTTTCCTATTCTATGTTGGTGATCTGCTGCTACACATACCTCATCTCTTCAAGTGC 360
Db 327 CTCAGTTTCCTATTCTATGTTGGTGATCTGCTGCTACACATACCTCATCTCTTCAAGTGC 386
Qy 361 AAAGACAAAGTGGAAATCTACAGAAAACTGCATGCTGTGGCTGCCAGTGTGGCATGTGG 420
Db 387 AAAGACAAAGTGGAAATCTACAGAAAACTGCATGCTGTGGCTGCCAGTGTGGCATGTGG 446
Qy 421 ACGTGTGATGTCATGTTGGTACCCCTGTTGCTCTCCCGTATGGAATCCATGAGGAA 480
Db 447 ACGTGTGATGTCATGTTGGTACCCCTGTTGCTCTCCCGTATGGAATCCATGAGGAA 506
Qy 481 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGGAATC 540
Db 507 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGGAATC 566
Qy 541 ATCAACTATATGATGATCTATTTTGTGCTATGAGCCGTTGCTGTGATCTGTGTTGCTTCCAG 600
Db 567 ATCAACTATATGATGATCTATTTTGTGCTATGAGCCGTTGCTGTGATCTGTGTTGCTTCCAG 626
Qy 601 GTCCTTCATCATATGATGATGCTGAGAGAGCTAGCCACTCTTTTACTATCCACACAGGAG 660
Db 627 GTCCTTCATCATATGATGATGCTGAGAGAGCTAGCCACTCTTTTACTATCCACACAGGAG 686
Qy 661 TTCTGGGCTCAGCTGAAAAAOCCTATTTTATAGGGTGCATCTTGTGTTGTTCTTCCC 720
Db 687 TTCTGGGCTCAGCTGAAAAAOCCTATTTTATAGGGTGCATCTTGTGTTGTTCTTCCC 746
Qy 721 TACCAGTTCTTTAGATCTATTTACTTGAATGTTGTGAGCGATTCATGCGCTGTAAACAGC 780
Db 747 TACCAGTTCTTTAGATCTATTTACTTGAATGTTGTGAGCGATTCATGCGCTGTAAACAGC 806
Qy 781 AAGGTTGCTATTTTAAACGAAATCTTCTTGAGTGTAAACAGCAATTTAGTCTATGATTTG 840
Db 807 AAGGTTGCTATTTTAAACGAAATCTTCTTGAGTGTAAACAGCAATTTAGTCTATGATTTG 866
Qy 841 CTTCTCTTTGCTTTGGGGAGACCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Db 867 CTTCTCTTTGCTTTGGGGAGACCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 926
Qy 901 TGTGTTTGTGCGGTTAG 918
Db 927 TGTGTTTGTGCGGTTAG 944

RESULT 9
US-10-292-798-1007
; Sequence 1007, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1007
; LENGTH: 113306
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source

FEATURE: (1)..(113306)
LOCATION: (1)..(113306)
NAME/KEY: CDS
LOCATION: (201)..(207)
FEATURE: (201)..(207)
NAME/KEY: CDS
LOCATION: (11526)..(12452)
FEATURE: (11526)..(12452)
NAME/KEY: CDS
LOCATION: (37954)..(38097)
FEATURE: (37954)..(38097)
NAME/KEY: CDS
LOCATION: (98732)..(98784)
FEATURE: (98732)..(98784)
NAME/KEY: CDS
LOCATION: (112891)..(113106)
FEATURE: (112891)..(113106)
US-10-292-798-1007
Query Match 100.0%; Score 918; DB 16; Length 113306;
Best Local Similarity 100.0%; Pred. No. 7,1e-269; Indels 0; Gaps 0;
Matches 918; Conservative 0; Mismatches 0;
Qy 1 ATCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGGGATCCCTATAGTGCACACCCCACTTA 60
Db 11540 ATCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGGGATCCCTATAGTGCACACCCCACTTA 11599
Qy 61 ATCAGCCTCTACTTCAATAGTGTCTTATTTGGGGCTGGTGGGTGTCATTTCCATCTCTTTC 120
Db 11600 ATCAGCCTCTACTTCAATAGTGTCTTATTTGGGGCTGGTGGGTGTCATTTCCATCTCTTTC 11659
Qy 121 CTCCTGGTGAATGAACACCCGGTCAGTGACACCATGGCGTCATTAACTTTGGTGGTG 180
Db 11660 CTCCTGGTGAATGAACACCCGGTCAGTGACACCATGGCGTCATTAACTTTGGTGGTG 11719
Qy 181 GTCACAGCGGTTTCTGTGACAGTGCCTATTTGGTGTGACCTCATCTCAAGAAAGACT 240
Db 11720 GTCACAGCGGTTTCTGTGACAGTGCCTATTTGGTGTGACCTCATCTCAAGAAAGACT 11779
Qy 241 TGGATGTTTGGGCTGCCCTCTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTAC 300
Db 11780 TGGATGTTTGGGCTGCCCTCTGCAAAATTTGTGAGTGCATGCTGCACATCCACATGTAC 11839
Qy 301 CTCACGTTCCATTTATGTTGATGTCCTGGTCAACAGATACCTCATCTTCTTCAAGTGC 360
Db 11840 CTCACGTTCCATTTATGTTGATGTCCTGGTCAACAGATACCTCATCTTCTTCAAGTGC 11899
Qy 361 AAAGACAAAGTGGAAATCTACAGAAAACTGCATGCTGTGGCTGCCAGTGTGGCATGTGC 420
Db 11900 AAAGACAAAGTGGAAATCTACAGAAAACTGCATGCTGTGGCTGCCAGTGTGGCATGTGC 11959
Qy 421 ACGTGTGATGTCATTTGTGTTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480
Db 11960 ACGTGTGATGTCATTTGTGTTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 12019
Qy 481 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAAAATC 540
Db 12020 TACAATGAGGACACTGTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAAAATC 12079
Qy 541 ATCAACTATATGATGATCTATTTTGTGATAGCGTTGTGATGCTGTGTTGTTCTTCCAG 600
Db 12080 ATCAACTATATGATGATCTATTTTGTGATAGCGTTGTGATGCTGTGTTGTTCTTCCAG 12139
Qy 601 GTCTTCATCATATGATGATGTTGAGAGAGTACGCCACTCTTTTACTATCCACACAGGAG 660
Db 12140 GTCTTCATCATATGATGATGTTGAGAGAGTACGCCACTCTTTTACTATCCACACAGGAG 12199
Qy 661 TTCTGGGCTCAGCTGAAAAAOCCTATTTTATAGGGGTGATCCTCTGTTGTTGTTCTTCCC 720
Db 12200 TTCTGGGCTCAGCTGAAAAAOCCTATTTTATAGGGGTGATCCTCTGTTGTTGTTCTTCCC 12259
Qy 721 TACCAGTTCTTTAGGATCTATTTACTTGAATGTTGTGAGCGATTCCTCAATGCCTGTAACAGC 780

```

; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1193
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1318)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1118)
; US-10-017-161-1193

Query Match      100.0%; Score 918; DB 15; Length 1318;
Best Local Similarity 100.0%; Pred. No. 3.5e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGCGATCCCTATAGTGACACCCACCTTA 60
DB 201 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGCGATCCCTATAGTGACACCCACCTTA 260

QY 61 ATCAGGCTCTACTTCTATAGTGTCTATTGGCGGCTGGTGGTGTCTATTTCCATTCTTTTC 120
DB 261 ATCAGGCTCTACTTCTATAGTGTCTATTGGCGGCTGGTGGTGTCTATTTCCATTCTTTTC 320

QY 121 CTCCTGGTGAANAATGAACCCCGTCACTGACACCAATGCGGTCAATTAATCTGGTGGTG 180
DB 321 CTCCTGGTGAANAATGAACCCCGTCACTGACACCAATGCGGTCAATTAATCTGGTGGTG 380

QY 181 GTCCACAGCGTTTCTGCTGACAGTGCCATTTTCGCTGACCTTACCTCATCAAGAGACT 240
DB 381 GTCCACAGCGTTTCTGCTGACAGTGCCATTTTCGCTGACCTTACCTCATCAAGAGACT 440

QY 241 TGGATGTTGGGCTGGCCCTTCTGCAATTTGTGAGTGCCCATGCTGCATCCACATGTATC 300
DB 441 TGGATGTTGGGCTGGCCCTTCTGCAATTTGTGAGTGCCCATGCTGCATCCACATGTATC 500

QY 301 CTCACGTTCTCTATTCTATGTTGTTGATCTGCTGACAGATACCTCTCTTCAAGTGC 360
DB 501 CTCACGTTCTCTATTCTATGTTGTTGATCTGCTGACAGATACCTCTCTTCAAGTGC 560

QY 361 AAAGACAAAGTGAATTTCTACAGAAATCTGCTGTGCTGCCAGTGTGCTGCTGCTGCTG 420
DB 561 AAAGACAAAGTGAATTTCTACAGAAATCTGCTGTGCTGCCAGTGTGCTGCTGCTGCTG 620

QY 421 ACCTGTGTGATGTTCTATGTTGGTGTACCCCTGTTGTCTCCCGTATGGAATCCATGAGAA 480
DB 621 ACCTGTGTGATGTTCTATGTTGGTGTACCCCTGTTGTCTCCCGTATGGAATCCATGAGAA 680

QY 481 TACAATGAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGCTTTACACATATGTGAAATC 540
DB 681 TACAATGAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGCTTTACACATATGTGAAATC 740

QY 541 ATCAACTATATGATGATCATTTTGTATAGCCGTTGCTGTGATTTCTGTTGTTCTTCCAG 600
DB 741 ATCAACTATATGATGATCATTTTGTATAGCCGTTGCTGTGATTTCTGTTGTTCTTCCAG 800

QY 601 GTCTTCATCATATTGTTGATGTGTGCAAGCTACGCCACTCTTTACTATATCCACACAGGAG 660
DB 801 GTCTTCATCATATTGTTGATGTGTGCAAGCTACGCCACTCTTTACTATATCCACACAGGAG 860

QY 661 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTGATCTCTGTTGTTGTTCTTCCCTCC 720
DB 861 TTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTGATCTCTGTTGTTGTTCTTCCCTCC 920

QY 721 TACCAGTTCCTTAGGATCTATTACTTGAATTTGTGACGCAATCCCAATGCTGTAAACAGC 780
DB 921 TACCAGTTCCTTAGGATCTATTACTTGAATTTGTGACGCAATCCCAATGCTGTAAACAGC 980

QY 781 AAGTTGCATTTTATACGAATCTTCTTGAGTGTAAACAGCAATTAGCTGTATGATTTG 840
DB 981 AAGTTGCATTTTATACGAATCTTCTTGAGTGTAAACAGCAATTAGCTGTATGATTTG 1040
```

```

QY 841 CTTCTCTTTGTCTTTTGGGGAAGCCATTGTTTAAAGCAAAAGATAAATTGCTCTATGCAAT 900
DB 1041 CTTCTCTTTGTCTTTTGGGGAAGCCATTGTTTAAAGCAAAAGATAAATTGCTCTATGCAAT 1100

QY 901 TGTCTTTTGTGCGGTAG 918
DB 1101 TGTCTTTTGTGCGGTAG 1118

RESULT 8
US-09-782-974C-81
; Sequence 81, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Patodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 2525
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-782-974C-81

Query Match      100.0%; Score 918; DB 10; Length 2525;
Best Local Similarity 100.0%; Pred. No. 5.5e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGCGATCCCTATAGTGACACCCACCTTA 60
DB 27 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGCGATCCCTATAGTGACACCCACCTTA 86

QY 61 ATCAGGCTCTACTTCTATAGTGTCTATTGGCGGCTGGTGGTGTCAATTTCCATTCTTTTC 120
DB 87 ATCAGGCTCTACTTCTATAGTGTCTATTGGCGGCTGGTGGTGTCAATTTCCATTCTTTTC 146

QY 121 CTCCTGGTGAANAATGAACCCCGTCACTGACACCAATGCGGTCAATTAATCTGGTGGTG 180
DB 147 CTCCTGGTGAANAATGAACCCCGTCACTGACACCAATGCGGTCAATTAATCTGGTGGTG 206

QY 181 GTCCACAGCGTTTCTGCTGACAGTGCCATTTTCGCTTACCTTACCTCATCAAGAGACT 240
DB 207 GTCCACAGCGTTTCTGCTGACAGTGCCATTTTCGCTTACCTTACCTCATCAAGAGACT 266

QY 241 TGGATGTTGGGCTGGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCATGTATC 300
```


361	AAAGCAAAGTGGAAATTTCTACAGAAA	CTGCTGCTGCCAGTCTGCTGGCATGTGG	420
421	ACGCTGGTGATTGTCAATTTGTGTACCCCTCGTGTCTCCCGGTATGGAATCCATAGAGAA	480	
421	ACGCTGGTGATTGTCAATTTGTGTGTAACCCCTGGTGTCTCCCGGTATGGAATCCATAGAGAA	480	
481	TACAAATGAGGACACATGTTTTAAATTTTACAAAAGAGCTTGCTTACACATATGTGAAATTC	540	
481	TACAAATGAGGACACATGTTTTAAATTTTACAAAAGAGCTTGCTTACACATATGTGAAATTC	540	
541	ATCAACTATATATAGTATCATTTTGTGCATAGCCGTGCTGTGATCTGTGGTCTTCCAG	600	
541	ATCAACTATATAGTATCATTTTGTGCATAGCCGTGCTGTGATCTGTGGTCTTCCAG	600	
601	GTCTTCATCATTTATGTGTGATGGTGAGAAGCTAGCCACTCTTTACTATCCCAACCAAGAG	660	
601	GTCTTCATCATTTATGTGTGATGGTGAGAAGCTAGCCACTCTTTACTATCCCAACCAAGAG	660	
661	TTCTGGGCTCAGCTGAAAACCTATTTTTTATAGGGTCACTCTTTGTTGTTTCCTTCCC	720	
661	TTCTGGGCTCAGCTGAAAACCTATTTTTTATAGGGTCACTCTTTGTTGTTTCCTTCCC	720	
721	TACCAGTCTCTTTAGGATCTATTACTTGTAATGTTGTGACGATTCCTCAATGCTCTAACAG	780	
721	TACCAGTCTCTTTAGGATCTATTACTTGTAATGTTGTGACGATTCCTCAATGCTCTAACAG	780	
781	AAGGTTGCATTTTATAACGAATCTCTTGAGTGTAACGCAATAGCTGCTATGATTG	840	
781	AAGGTTGCATTTTATAACGAATCTCTCTGAGTGTAAACAGCAATTAGCTCTATGATTG	840	
841	CTTCTCTTTGTCCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT	900	
841	CTTCTCTTTGTCCTTTGGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT	900	
901	TGTGTTTTGTGCGGTAG	918	
901	TGTGTTTTGTGCGGTAG	918	

RESIT.T 6

```

US-10-293-171-1.
; Sequence 1, Application US/10293171
; Publication No. US20030138418A1
; GENERAL INFORMATION:
; APPLICANT: Eishingdrello, Haifeng
; APPLICANT: Cai, Jidong
; APPLICANT: Gassenhuber, Johann
; TITLE OF INVENTION: A NUCLEIC ACID NP
; FILE REFERENCE: USA2001/0158 US
; CURRENT APPLICATION NUMBER: US/10/293,171
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US60/354,150
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-293-171-1

```

Query Match	100.0%	Score 918;	DB 15;	Length 1040;
Best Local Similarity	100.0%	Pred. No. 3e-270;		
Matches 918:	Conservative	0;	Mismatches 0;	Indels 0;
Gaps				

[illegible]

RESULT 7

RESUL 1 /
 US-10-017-161-1193
 ; Sequence 1193, Application US/10017161
 ; Publication No. US20030143668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUWA, MAKIKO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: ABURATANI, HIROYUKI
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 084339/0152
 ; CURRENT APPLICATION NUMBER: US/10/017,161
 ; CURRENT FILING DATE: 2002-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001/246789
 ; PRIOR FILING DATE: 2001-06-18

Qy	121	CTCTCGGTGAAAATGAAACACCGGTGAGTGACCAACCATGGCGGTCAATTAACCTTGGTGGT	180
Db	121	CTCTCGGTGAAAATGAAACACCGGTGAGTGACCAACCATGGCGGTCAATTAACCTTGGTGGT	180
Qy	181	GTCCACACGCGTTTTCTGCTTGACAGTGCCTATTTGCTTGACCTTACCTCATCAAGAAGACT	240
Db	181	GTCCACACGCGTTTTCTGCTTGACAGTGCCTATTTGCTTGACCTCATCAAGAAGACT	240
Qy	241	TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCCATGCTGCACATCCACATGTAC	300
Db	241	TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCCATGCTGCACATCCACATGTAC	300
Qy	301	CTCAGGTTCTTATTTCTATGTGGTGATCCTGGTCACAGATACCTCATCTTCTCAAGTGC	360
Db	301	CTCAGGTTCTTATTTCTATGTGGTGATCCTGGTCACAGATACCTCATCTTCTCAAGTGC	360
Qy	361	AAAGACAAAGTGGAAATCTACAGAAAACTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG	420
Db	361	AAAGACAAAGTGGAAATCTACAGAAAACTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG	420
Qy	421	AGCTGGTGATGTGCTATTTGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA	480
Db	421	AGCTGGTGATGTGCTATTTGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA	480
Qy	481	TACAAATGAGGAGCACTGTTTTAAATTTTACAAAAGAGCTTCTTTACACATATGTGAAAATC	540
Db	481	TACAAATGAGGAGCACTGTTTTAAATTTTACAAAAGAGCTTCTTTACACATATGTGAAAATC	540
Qy	541	ATCAACTATATGATAGTCAATTTTTGTCAAGCCGTTGCTGTGATCTGTGGTCTTCCAG	600
Db	541	ATCAACTATATGATAGTCAATTTTTGTCAAGCCGTTGCTGTGATCTGTGGTCTTCCAG	600
Qy	601	GTCTTCATCATATGTTGATGGTCAGAAAGCTACGCCACTCTTTACTATCCCAACCAAGAG	660
Db	601	GTCTTCATCATATGTTGATGGTCAGAAAGCTACGCCACTCTTTACTATCCCAACCAAGAG	660
Qy	661	TTCTCGGCTCAGCTGAAAACCTATTTTTATAGGGGTCACTCTGTTGTTTCTTCCCTCCC	720
Db	661	TTCTCGGCTCAGCTGAAAACCTATTTTTATAGGGGTCACTCTGTTGTTTCTTCCCTCCC	720
Qy	721	TACCAAGTCTTTAGATCTATTACTTGAAATTTGTGTGACGCATTCCTCAATGCTGTAAACAGC	780
Db	721	TACCAAGTCTTTAGATCTATTACTTGAAATTTGTGTGACGCATTCCTCAATGCTGTAAACAGC	780
Qy	781	AGGTTTGCAATTTTATAAGCAATCTCTTCGAGTGTAACAGCAATTAGCTGCTATGATTTG	840
Db	781	AGGTTTGCAATTTTATAAGCAATCTCTTCGAGTGTAACAGCAATTAGCTGCTATGATTTG	840
Qy	841	CTTCTCTTTGTCTTTGGGGGAAGCCATTTGGTTTAAAGCAAAAGATAATTGGCTTTATGGAAT	900
Db	841	CTTCTCTTTGTCTTTGGGGGAAGCCATTTGGTTTAAAGCAAAAGATAATTGGCTTTATGGAAT	900
Qy	901	TGTGTTTGTGCCGTTAG 918	
Db	901	TGTGTTTGTGCCGTTAG 918	

```
; Sequence 1, Application US/10055106C
; Publication No. US20030017536A1
; GENERAL INFORMATION:
; APPLICANT: Harland, Lee
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PC10970AGLK
; CURRENT APPLICATION NUMBER: US/10/055,106C
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: GB0101739.1
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/267,341
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-055-106c-1

Query Match 100.0%; Score 918; DB 13; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.8e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGGATCCTATAGTGACACCCCACTTA 60
DB 1 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGGATCCTATAGTGACACCCCACTTA 60
QY 61 ATCAGCTCTACTTATAGTGCCTTATTTGGGGCTGGTGGTGTCTATTTCCATTTCTTTTC 120
DB 61 ATCAGCTCTACTTATAGTGCCTTATTTGGGGCTGGTGGTGTCTATTTCCATTTCTTTTC 120
QY 121 CTCTGGTGAATAATGAACACCCGGTGTGACACCAATGCGGTCAATTAACCTGGTGGTG 180
DB 121 CTCTGGTGAATAATGAACACCCGGTGTGACACCAATGCGGTCAATTAACCTGGTGGTG 180
QY 181 GTCCACAGCGTTTCTGCTGACAGTGCATTTGCGTGTGACCTACCTCATCAAGAAGACT 240
DB 181 GTCCACAGCGTTTCTGCTGACAGTGCATTTGCGTGTGACCTACCTCATCAAGAAGACT 240
QY 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCGCATCCACATGTAC 300
DB 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCGCATCCACATGTAC 300
QY 301 CTCACGTTCCCTATTCTATGTGTGATCCTGTGTCCACAGATACCTCATCTTCAAGTGC 360
DB 301 CTCACGTTCCCTATTCTATGTGTGATCCTGTGTCCACAGATACCTCATCTTCAAGTGC 360
QY 361 AAAGAACAAGTGAATTTCTACAGAAACTGCTGTGGTGGCTGCGAGTGGCATGTGG 420
DB 361 AAAGAACAAGTGAATTTCTACAGAAACTGCTGTGGTGGCTGCGAGTGGCATGTGG 420

; Sequence 9, Application US/10188405
; Publication No. US20030082585A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Dai, Kang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Zhao, Jiagang
; APPLICANT: Cusler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030082585A1e1 Receptors
; FILE REFERENCE: 019781-008410US
; CURRENT APPLICATION NUMBER: US/10/188,405
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR343
; US-10-188-405-9

Query Match 100.0%; Score 918; DB 15; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.8e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGGATCCTATAGTGACACCCCACTTA 60
DB 1 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGGATCCTATAGTGACACCCCACTTA 60
QY 61 ATCAGCTCTACTTATAGTGCCTTATTTGGGGCTGGTGGTGTCTATTTCCATTTCTTTTC 120
DB 61 ATCAGCTCTACTTATAGTGCCTTATTTGGGGCTGGTGGTGTCTATTTCCATTTCTTTTC 120
QY 121 CTCCTGGTGAATAATGAACACCCGGTGTGACACCAATGCGGTCAATTAACCTGGTGGTG 180
DB 121 CTCCTGGTGAATAATGAACACCCGGTGTGACACCAATGCGGTCAATTAACCTGGTGGTG 180
QY 181 GTCCACAGCGTTTCTGCTGACAGTGCATTTGCGTGTGACCTACCTCATCAAGAAGACT 240
DB 181 GTCCACAGCGTTTCTGCTGACAGTGCATTTGCGTGTGACCTACCTCATCAAGAAGACT 240
QY 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCGCATCCACATGTAC 300
DB 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCGCATCCACATGTAC 300
QY 301 CTCACGTTCCCTATTCTATGTGTGATCCTGTGTCCACAGATACCTCATCTTCAAGTGC 360
DB 301 CTCACGTTCCCTATTCTATGTGTGATCCTGTGTCCACAGATACCTCATCTTCAAGTGC 360
QY 361 AAAGAACAAGTGAATTTCTACAGAAACTGCTGTGGTGGCTGCGAGTGGCATGTGG 420
DB 361 AAAGAACAAGTGAATTTCTACAGAAACTGCTGTGGTGGCTGCGAGTGGCATGTGG 420
```

241 TGGATGTTTGGCTGCCCTTCTGCAAAATTGTGAGTGCCATGCTGCACATCCACATGTAC 300
241 TGGATGTTTGGCTGCCCTTCTGCAAAATTGTGAGTGCCATGCTGCACATCCACATGTAC 300
301 CTCAGCTTCTATCTATGTGTGTATCTCTGTCACAGATACCTCACTTCTTCAAGTGC 360
301 CTCAGCTTCTATCTATGTGTGTATCTCTGTCACAGATACCTCACTTCTTCAAGTGC 360
361 AAAGCAAAAGTGGAAATCTTACAGAAATCTGTCAGTGTGCTGCGCAGTGTGCAATGCAAGAA 420
361 AAAGCAAAAGTGGAAATCTTACAGAAATCTGTCAGTGTGCTGCGCAGTGTGCAATGCAAGAA 420
421 AGCTGGTGAATGTCATGTGTGTACCCCTGCTGTCAGTGTGCTGCGCAGTGTGCAATGCAAGAA 480
421 AGCTGGTGAATGTCATGTGTGTACCCCTGCTGTCAGTGTGCTGCGCAGTGTGCAATGCAAGAA 480
481 TACAATGAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGTCTACATATGTGAAATC 540
481 TACAATGAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGTCTACATATGTGAAATC 540
541 ATCAACTATATGATGTATGTTTGTATGAGCGCTTGTCTGATCTGTTGCTTCTCCAG 600
541 ATCAACTATATGATGTATGTTTGTATGAGCGCTTGTCTGATCTGTTGCTTCTCCAG 600
601 GTCTTCATCATATGTTGATGTGAGAGCTACCGCCTCTTACTATCCACAGAG 660
601 GTCTTCATCATATGTTGATGTGAGAGCTACCGCCTCTTACTATCCACAGAG 660
661 TTCTGGGCTCAGTGAACCACTATTTTATAGGGGTGATCTCTGTTGTTTCTCTCC 720
661 TTCTGGGCTCAGTGAACCACTATTTTATAGGGGTGATCTCTGTTGTTTCTCTCC 720
721 TACCAAGTCTTATGAGTATCTTACTGTAATGTGTGAGCGCATTCATGCTGTAAACAG 780
721 TACCAAGTCTTATGAGTATCTTACTGTAATGTGTGAGCGCATTCATGCTGTAAACAG 780
781 AAGGTGCAATTTTAAACCAATCTTCTGAGTGAACAGCAATAGCTGTATGATTTG 840
781 AAGGTGCAATTTTAAACCAATCTTCTGAGTGAACAGCAATAGCTGTATGATTTG 840
841 CTCTCTTCTTCTTGGGGAAGCCATTCGTTTAAAGCAAAAGATATGCTTATGGAAT 900
841 CTCTCTTCTTCTTGGGGAAGCCATTCGTTTAAAGCAAAAGATATGCTTATGGAAT 900
901 TGTGTTTGTGCGGTAG 918
901 TGTGTTTGTGCGGTAG 918

RESULT 3
US-10-297-908A-2
; Sequence 2, Application US/10297908A
; Publication No. US20040029793A1
; GENERAL INFORMATION:
; APPLICANT: MORIYA, Takeo
; APPLICANT: ITO, Takahashi
; APPLICANT: SHINJANI, Yasushi
; APPLICANT: MIYAJIMA, No. US20040029793A1yuyuki
; TITLE OF INVENTION: No. US20040029793A1 G Protein-Coupled Receptor Protein and its
; FILE REFERENCE: 2737 USOP
; CURRENT APPLICATION NUMBER: US/10/297,908A
; CURRENT FILING DATE: 2002-12-11
; PRIOR FILING DATE: PCT/JP01/05061
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: JP 2000-184596
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: JP 2000-223887
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Human

US-10-297-908A-2
Query Match 100.0%; Score 918; DB 13; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.8e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTTGGATCCTATAGTAGACACCCCACTTA 60
Db 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTCTTGGATCCTATAGTAGACACCCCACTTA 60
Qy 61 ATCAGCCTCTACTTCTATAGTGTCTTATTTGGGGGCTGTGTGGGTGTCATTTCCATTTCTTTC 120
Db 61 ATCAGCCTCTACTTCTATAGTGTCTTATTTGGGGGCTGTGTGGGTGTCATTTCCATTTCTTTC 120
Qy 121 CTCCTGTGAAATGAACACCCCGTCACTGACCAACATGCGGTGCTAATACTTGGTGTG 180
Db 121 CTCCTGTGAAATGAACACCCCGTCACTGACCAACATGCGGTGCTAATACTTGGTGTG 180
Qy 181 GTCCACAGCCCTTTTCTGCTGACAGTGCCTATTTGCTTGGCTTACCTCATCAAGAAAGACT 240
Db 181 GTCCACAGCCCTTTTCTGCTGACAGTGCCTATTTGCTTGGCTTACCTCATCAAGAAAGACT 240
Qy 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCAACATCCACATGTAC 300
Db 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCAACATCCACATGTAC 300
Qy 301 CTCAGCTTCTATGTTGATGTGCTGTCACCAAGATACCTCATCTTCTTCAAGTGC 360
Db 301 CTCAGCTTCTATGTTGATGTGCTGTCACCAAGATACCTCATCTTCTTCAAGTGC 360
Qy 361 AAAGCAAAAGTGGAAATCTACAGAAATCTGATGCTGTGCTGCGCAGTGTGCAATGCAAGAA 420
Db 361 AAAGCAAAAGTGGAAATCTACAGAAATCTGATGCTGTGCTGCGCAGTGTGCAATGCAAGAA 420
Qy 421 ACGTGTGATGTGATGTGTTACCCCTGCTGTCCTCCGCTATGGAATCCATGAGAA 480
Db 421 ACGTGTGATGTGATGTGTTACCCCTGCTGTCCTCCGCTATGGAATCCATGAGAA 480
Qy 481 TACAATGAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGTCTACACATATGCAAAATC 540
Db 481 TACAATGAGGAGCAGCTGTTTAAATTTTCAAAAGAGCTTGTCTACACATATGCAAAATC 540
Qy 541 ATCAACTATATGATGTATGTTTGTATAGCCCTTGTCTGTGATCTTGTGTTTCTTCCAG 600
Db 541 ATCAACTATATGATGTATGTTTGTATAGCCCTTGTCTGTGATCTTGTGTTTCTTCCAG 600
Qy 601 GTCTTCATCATATGTTGATGTGAGAGCTACCGCCTCTTACTATCCACAGAG 660
Db 601 GTCTTCATCATATGTTGATGTGAGAGCTACCGCCTCTTACTATCCACAGAG 660
Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTGATCTCTTGTTCCTTCCC 720
Db 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTGATCTCTTGTTCCTTCCC 720
Qy 721 TACAGATCTTATAGATCTATTAAGTGTGTGAGCGATTCCTCAATGCTGTAAACAG 780
Db 721 TACAGATCTTATAGATCTATTAAGTGTGTGAGCGATTCCTCAATGCTGTAAACAG 780
Qy 781 AAGGTGCAATTTTAAACCAATCTTCTGAGTGAACAGCAATAGCTGTATGATTTG 840
Db 781 AAGGTGCAATTTTAAACCAATCTTCTGAGTGAACAGCAATAGCTGTATGATTTG 840
Qy 841 CTCTCTTGTCTTGGGGAAGCCATTCGTTTAAAGCAAAAGATATGCTTATGGAAT 900
Db 841 CTCTCTTGTCTTGGGGAAGCCATTCGTTTAAAGCAAAAGATATGCTTATGGAAT 900
Qy 901 TGTGTTTGTGCGGTAG 918
Db 901 TGTGTTTGTGCGGTAG 918

RESULT 4
US-10-055-106C-1

;; PRIOR APPLICATION NUMBER: 60/309,208
;; PRIOR FILING DATE: 2001-07-31
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 918
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; US-09-995-225-3

Query Match 100.0%; Score 918; DB 9; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.8e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTTGGATCCTATAGTACACCCCACTTA 60
DB 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTTGGATCCTATAGTACACCCCACTTA 60

QY 61 ATCAGCTCTACTTCTATAGTGTCTTATTTGGGGGCTGGTGGTGTCTATTTCCATTCCTTTTC 120
DB 61 ATCAGCTCTACTTCTATAGTGTCTTATTTGGGGGCTGGTGGTGTCTATTTCCATTCCTTTTC 120

QY 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAACATGCGGTGCTATTAACCTTGGTGGTG 180
DB 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAACATGCGGTGCTATTAACCTTGGTGGTG 180

QY 181 GTCCACAGCGTTTCTCTGCTGACAGTGCATTTGGCTTGACCTACCTCATCAAGAGACT 240
DB 181 GTCCACAGCGTTTCTCTGCTGACAGTGCATTTGGCTTGACCTACCTCATCAAGAGACT 240

RESULT 2

US-09-995-225-3
; Sequence 3, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:

; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pridie, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-995-225-3

Query Match 100.0%; Score 918; DB 10; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.8e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTTGGATCCTATAGTACACCCCACTTA 60
DB 1 ATGCTGGCCACAAATACCTCCAGAAATTCCTTTGGATCCTATAGTACACCCCACTTA 60

QY 61 ATCAGCTCTACTTCTATAGTGTCTTATTTGGGGGCTGGTGGTGTCTATTTCCATTCCTTTTC 120
DB 61 ATCAGCTCTACTTCTATAGTGTCTTATTTGGGGGCTGGTGGTGTCTATTTCCATTCCTTTTC 120

QY 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAACATGCGGTGCTATTAACCTTGGTGGTG 180
DB 121 CTCCTGTGAAATGAACACCCGGTCACTGACCAACATGCGGTGCTATTAACCTTGGTGGTG 180

QY 181 GTCCACAGCGTTTCTCTGCTGACAGTGCATTTGGCTTGACCTACCTCATCAAGAGACT 240
DB 181 GTCCACAGCGTTTCTCTGCTGACAGTGCATTTGGCTTGACCTACCTCATCAAGAGACT 240

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 15:41:59 ; Search time 460 Seconds
(without alignments)
8997.651 Million cell updates/sec

Title: US-10-055-106C-1

Perfect score: 918

Sequence: 1 atgcctgccacaatcctc.....attgtgtttgtgcggttag 918

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/FCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	9	US-09-995-225-3
2	918	100.0	918	10	US-09-995-225-3
3	918	100.0	918	13	US-10-297-908A-2
4	918	100.0	918	13	US-10-055-106C-1
5	918	100.0	918	15	US-10-188-405-9
6	918	100.0	1040	15	US-10-293-171-1
7	918	100.0	1318	15	US-10-017-161-1193
8	918	100.0	2525	15	US-09-782-974C-81
9	918	100.0	113306	16	US-10-292-798A-81
10	916.4	99.8	1684	15	US-10-085-233B-1
11	913.4	99.5	939	15	US-10-085-233B-3
12	560.8	61.1	810	15	US-10-366-504-1
13	390	42.5	447	10	US-09-782-974C-21
14	76.4	8.3	1113	11	US-09-826-509-540

ALIGNMENTS

RESULT 1

US-09-995-225-3
; Sequence 3, Application US/0995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Priddy, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14

76.4 8.3 1805 9 US-09-823-114-18
76.4 8.3 1805 15 US-10-290-748-18
76.4 8.3 1829 10 US-09-905-186A-9
76.4 8.3 1829 10 US-09-905-186A-10
76.4 8.3 1829 10 US-09-905-186A-11
76.4 8.3 1973 16 US-10-305-720-1391
76.4 8.3 2534 15 US-10-087-345A-22
76.4 8.3 2534 15 US-10-225-567A-208
76.4 8.3 2534 16 US-10-352-684A-31
76.4 8.3 2534 16 US-09-905-186A-7
76.4 8.3 2534 16 US-09-905-186A-8
76.4 8.3 2534 16 US-09-905-186A-1
76.4 8.3 2534 16 US-09-905-186A-2
76.4 8.3 2534 16 US-09-905-186A-3
76.4 8.3 2534 16 US-09-905-186A-4
76.4 8.3 2534 16 US-09-905-186A-5
76.4 8.3 2534 16 US-09-905-186A-6
76.4 8.3 2534 16 US-09-905-186A-7
76.4 8.3 2534 16 US-09-905-186A-8
76.4 8.3 2534 16 US-09-905-186A-9
76.4 8.3 2534 16 US-09-905-186A-10
76.4 8.3 2534 16 US-09-905-186A-11
76.4 8.3 2534 16 US-09-905-186A-12
76.4 8.3 2534 16 US-09-905-186A-13
76.4 8.3 2534 16 US-09-905-186A-14
76.4 8.3 2534 16 US-09-905-186A-15
76.4 8.3 2534 16 US-09-905-186A-16
76.4 8.3 2534 16 US-09-905-186A-17
76.4 8.3 2534 16 US-09-905-186A-18
76.4 8.3 2534 16 US-09-905-186A-19
76.4 8.3 2534 16 US-09-905-186A-20
76.4 8.3 2534 16 US-09-905-186A-21
76.4 8.3 2534 16 US-09-905-186A-22
76.4 8.3 2534 16 US-09-905-186A-23
76.4 8.3 2534 16 US-09-905-186A-24
76.4 8.3 2534 16 US-09-905-186A-25
76.4 8.3 2534 16 US-09-905-186A-26
76.4 8.3 2534 16 US-09-905-186A-27
76.4 8.3 2534 16 US-09-905-186A-28
76.4 8.3 2534 16 US-09-905-186A-29
76.4 8.3 2534 16 US-09-905-186A-30
76.4 8.3 2534 16 US-09-905-186A-31
76.4 8.3 2534 16 US-09-905-186A-32
76.4 8.3 2534 16 US-09-905-186A-33
76.4 8.3 2534 16 US-09-905-186A-34
76.4 8.3 2534 16 US-09-905-186A-35
76.4 8.3 2534 16 US-09-905-186A-36
76.4 8.3 2534 16 US-09-905-186A-37
76.4 8.3 2534 16 US-09-905-186A-38
76.4 8.3 2534 16 US-09-905-186A-39
76.4 8.3 2534 16 US-09-905-186A-40
76.4 8.3 2534 16 US-09-905-186A-41
76.4 8.3 2534 16 US-09-905-186A-42
76.4 8.3 2534 16 US-09-905-186A-43
76.4 8.3 2534 16 US-09-905-186A-44
76.4 8.3 2534 16 US-09-905-186A-45

assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source
1. .661
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630103H01"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells"

ORIGIN

Query Match 9.1%; Score 83.6; DB 13; Length 661;
Best Local Similarity 76.7%; Pred. No. 1.4e-11;
Matches 115; Conservative 0; Mismatches 34; Indels 1; Gaps 1;
QY 1 ATGCTGGCCACAAATCCCTCCAGGAATCTCTTGGCATCTCTATAGTGACACCCACTTGA 60
Db 513 ATGGATGGATATAATACCTCTGAGAAATCTCTTGTGACCTATATCTGGCACACCACTTA 572
QY 61 ATCAGCCTCTACTTCATAGTGGCTTATTTGGGGCTGGTGGTGTCTATTTCCATTCTTTTC 120
Db 573 ACATGATTTACTTCATAGTGGCTTCATTTGAGGAGCTGGTAGGCTCATCTCCATCCTGTTTC 632
QY 121 CTCCTCGTGAATAATGAACCCCGTCAGTG 150
Db 633 TTGCTGGTG-AAATGAACCTCACGTTTCAGTG 661

RESULT 15

CD469227
LOCUS
DEFINITION
LeukoS2_2_H07.q1.A024 Stimulated peripheral blood leukocytes S2
Equis caballus cDNA clone LeukoS2_2_H07_A024 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Equis caballus (horse)
Equis caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE
AUTHORS
Vandenplas,M., Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S.,
Moore,J.N., Liang,C., Sun,F., Sullivan,R., Shah,M. and Pratt,L.H.
TITLE
An EST database from equine (Equis caballus) stimulated peripheral
blood leukocytes
JOURNAL
COMMENT
Unpublished (2003)
Other ESTs: LeukoS2_2_H07.bl.A024
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; tissue and RNA were prepared in the Department of Large
Animal Medicine, University of Georgia; sequencing done in the
Laboratory for Genomics and Bioinformatics, University of Georgia.
Sequence ends have been trimmed to exclude vector and regions below
phred quality 16. Three-prime sequences are presented as their
reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).

FEATURES

source
1. .679
Location/Qualifiers
/organism="Equis caballus"
/mol_type="mRNA"
/strain="thoroughbred"
/db_xref="taxon:9796"

/clone="LeukoS2_2_H07_A024"
/sex="male"
/tissue_type="blood"
/cell_type="leukocytes"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Stimulated peripheral blood leukocytes S2"
/note="Organ: circulatory system; Vector: pME18S-FL3;
Site 1: XhoI; Site 2: XhoI; The library was prepared from
polyA+ RNA from equine peripheral blood leukocytes
isolated from a healthy adult horse. The leukocytes were
stimulated for 4 hr with 10 ng/ml E. coli O55:85 LPS.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 8.5%; Score 77.8; DB 14; Length 679;
Best Local Similarity 49.9%; Pred. No. 5.4e-10;
Matches 255; Conservative 0; Mismatches 247; Indels 9; Gaps 2;
QY 361 AAAGACAAAGTGAATTTCTACAGAAACTGCATGCTGTGGCTGCCAGTGTGGCATGTGG 420
Db 35 AAACCTCAACTGCCAACAGTTAAAAAAGTACCAGTGGGTAGTTTAAAGCATTATTATTGG 94
QY 421 ACGCTGTGATGTGATGTGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480
Db 95 ATAGTGGGTAGCCTTATTTTGGCCAAATATTTCTTTTACTATATGSCAAGTACAAAGT 154
QY 481 TACAATGAGGAGCA---CTGTTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAA 537
Db 155 TACTCAGACAGCAACGATGCTTTGAGTTCTACAAGACTTCAACACACAGGAATTCATC 214
QY 538 ATCATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
Db 215 ATCTTGAATTAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 274
QY 598 CAGCTCTTCATCATATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 657
Db 275 CAGATGGGTGTCATGTTCACTCATAAAGTCTTTGGCTGACCTGTGGGCTCATCAA 334
QY 658 GAGTTCTGGGCTCAGCTGAAACCTATTTTATAGGGGTGATCTCTTGTGTTTGTTCCTT 717
Db 335 GAGTATAGAGCTCAAAATCAAGAGCTGCTTCTCTCTAGTAATAGTGTCTGTCTGTTTATA 394
QY 718 CCCTACCAAGTCTTTAGGATCTATTTACTTGAATGTTGTGAGCGATTCCTCAATGCTGTAAC 777
Db 395 CCCACCATGATTCGGGTACACT-----TTCCTCAGATTTATTCAGAGGGAGAAAT 448
QY 778 AGCAAGGTTGCATTTTATACGAAATCTCTTGTAGTGTAAACAGCAATTAGCTGTATGAT 837
Db 449 TCTGAGTTAGTTCTTTATATGAATTTTGTGGCTTTAACTACTGTCTGTGCTGGAT 508
QY 838 TTGCTTCTTTGTTCTTTGGGGAGCCATT 868
Db 509 ATGCTGTGTTTCGTAGGTGGAGTTATCCATT 539

Search completed: April 25, 2004, 17:44:32
Job time : 2952 secs


```

/tissue_type="Skeletal white muscle, cardiac muscle,
kidney_brain, gill, intestinal mucosa"
/dev_stage="Adult"
/lab_host="E.coli Electromax DH10B"
/clone_lib="Carp mixed tissue library 2"
/notes="Vector: pTriplex2; Site 1: SfiI GGCCATCGGCC;
Site 2: SfiI GGCCCGCGGCC; Normalized and serially
subtracted cDNA library prepared from mixed tissues of
warm, cold and hypoxia challenged animals"

ORIGIN

Query Match 11.4%; Score 104.4; DB 14; Length 844;
Best Local Similarity 51.1%; Pred. No. 3e-17;
Matches 347; Conservative 322; Indels 10; Gaps 4;

QY 68 TCTACTTCATAGTCTTATTGGCGGCTGGTGGTGCATTTCCATTTCTCTCTCGG 127
DB 88 TATATATATTCACTTTCTGTGGGACTGTAATGTTGTAATGCTGCTGTAAGCTAC 147

QY 128 TGAATAATGAACACCGGTCACTGACACCACTAGGGGTCATTAATCTGGTGTGTCACCA 187
DB 148 AGTCCCAAGGGCTCTCTTTCCACCAAGTGTCTGTAATCAACTGATAGCAGTGCAC 207

QY 188 GCGTTTTTCTGCTGACAGTGCATTTGCTGTGACC---TACCTCATCAAGAGCTGG 243
DB 208 CCGTTTTTCTCTCACGGTGCCTTTTCGCAATTAATTAATGCTTTTAATAAGAGCTGG 267

QY 244 ATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCATCTGCGCATCCATCATATACCTC 303
DB 268 ATCTTGGCATACATTTCTGCAAAATTTGTCAGTATATGATCCATGCCACATGATCTT 327

QY 304 ACGTTCCTATTCTATGCTGATCTGCTGACCAATACCTCTCTCTCAAGTGCAGAA 363
DB 328 GCATTTATCTTCTATGCTTCTCTTAATTTGCGCTATCGGAGCGGTCTGTATCAACAA 387

QY 364 GACAAAGTGAATTTACAGAAAATCGCATGCTGTGGCTGCGCAGTGTGGCATGTGGACG 423
DB 388 CACAGCTAAAGTTTCATCGCATCTTTCAGCCAGATGTCAGTGCAGGCTCGA-- 445

QY 424 CTGCTGATGTCAATGTGGTACCCCTGTTGCTCCCGGATGATGAATCATGAGGATAC 483
DB 446 TGGTCTATATTCTGCTGATGATCCAGCAATGCTGTAATTTATGGAAT---GGCACAGAA 501

QY 484 AATGAGGAGCACTGTTTAAATTTTACAAAGAGCTGCTTACACATATGTGAAATCATC 543
DB 502 GATTCACATCTGTTTAAATTTTGGTCAGGCTCTCACCCAGCTACTGTGAAGACATTA 561

QY 544 AACTATATGATGATCAATTTTGTATAGCCGTTGCTGTGATCTGTTGGTCTTCCAGTTC 603
DB 562 AACTATGTAATTTGATATACTAATACTGTTTGGAGTGTCTGCGAGTCTTCCAAAT 621

QY 604 TTCATCATATGTTGATGCTGACAGAGTACGCCACTTTTACTATCCACCAGAGTTC 663
DB 622 TATTTCTGCTCAAGTGAGTAAACATTTGGAAGGCCCATGTCAACGTCAAGAGTTC 681

QY 664 TGGGCTCAGCTGAAAACTATTTTATAGGGTTCATCTTGTGTTTCTTCCCTAC 723
DB 682 TGGGCAACCACTGAAGAATGTTTCTCTGCTGTTGTTATGTTTGTGTTGCGCCCTA 741

QY 724 CAGTCTTTAGGATCTATT 742
DB 742 TCAGGATTCAGAGTGATT 760

```

```

RESULT 14
LOCUS BY748361 661 bp mRNA linear EST 17-DEC-2002
DEFINITION BY748361 RIKEN full-length enriched, NOD-derived CD11c +ve
dendritic cells Mus musculus cDNA clone F630103H01 5', mRNA
sequence.
ACCESSION BY748361
VERSION BY748361.1 GI:27177122
KEYWORDS EST.

```

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 661)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Shionobach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V.,
Ciothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,D., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Perteau,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,K., Itoh,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watanabe,A., Muramatsu,M. and Hayashizaki,Y.

TITLE

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome.res@sc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watanabe,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose

/dev stage="2-3 weeks old"
/clone lib="rikeni"
/notes="CB inbred strain"

ORIGIN

Query Match 15.5%; Score 142; DB 9; Length 834;
Best Local Similarity 64.1%; Pred. No. 1.5e-27;
Matches 225; Conservative 0; Mismatches 125; Indels 1; Gaps 1;
QY 57 CTTAATCAGCCTTACTTCAATGCTTATTTGGCGGCTGGTGGTGCATTTCATTTCAATTC 116
Db 438 CTTGATTACTGTCTACTCAGTTCCTTTGCTGGAGGTGGGATAGGATCCACTGCAATGTC 497
QY 117 TTTTCTCTCTGGTGAATGAACACCCGGTTCAGTGCACACATGGCGGTCAATTAACCTGGT 176
Db 498 ATTGTGCTGGTCAAGATGAACAGTCTGTCTGTGACACATCAAGCCATTAATTAATCTAGT 557
QY 177 GGTGGTCCACAGCGGTTTTCTGTCAGTGCACATTTGCGTTGACCTACCTCATCAAGAA 236
Db 558 TGTGGTACATGGTCTCCTCTCTCAGTGCCTTCCTGGTCTGCACTACTATGTCAATAA 617
QY 237 GACTTGGATGTTTTGGGCTGCGCTCTCTGCAATTTGTGAGTGCACCTGCTGCACATCCACAT 296
Db 618 GGAGTGGATCTTCCACATACCATCTCTGTAATGGTGGTGGTGGTGGTGGTGGTGGTGGT 677
QY 297 GTACCTCACGCTTCTATTCTATGTTGTTGATCTCTGTCACCGTCCAGATACCTCATC-TTCTTCA 355
Db 678 GTATTGACCTTCTATTCTACGTGATCACACTGGTGTATCCGCGGNGTGGGCTTCTTCTTC 737
QY 356 AGTGCAAGCAAGTGGATTTCTACAGAAATCTGATGCTGTGGTGGTGGTGGTGGTGGTGG 406
Db 738 AATGGAAGGACANGGTAGAGTTTTATAGAAAGTNCATGCCATTGCTTGCA 788

RESULT 12

CA355790 627748 NCCWA 1RT Oncorhynchus mykiss cdna clone 1RT88K09_A_F05 5',
LOCUS mRNA sequence.
DEFINITION CA355790
ACCESSION CA355790.1 GI:24600977
VERSION
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 680)
AUTHORS Rexroad, C.E. and Keele, J.W.
TITLE Sequence analysis of a rainbow trout normalized cdna library
JOURNAL Unpublished (2002)
COMMENT Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Lestown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing, bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross_match v0.990329.
Seq primer: AGCGGATACCAATTTCACAGGA.
Location/Qualifiers
1. .680
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="1RT88K09_A_F05"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="NCCWA 1RT"
/note="Vector: pCMV SPOT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."

FEATURES
source

ORIGIN

Query Match 12.1%; Score 111; DB 14; Length 680;
Best Local Similarity 55.9%; Pred. No. 4.3e-19;
Matches 210; Conservative 0; Mismatches 166; Indels 0; Gaps 0;
QY 110 CCATTCTTTCTCTCTGTAATAATGAACACCCCGTTCAGTGACCCACCATGCGCGTCAATTA 169
Db 305 CCTGATGATCCACATCTCCATCCAAATCCAAATGCGATCAGTATCACCATCGTATGCTCA 364
QY 170 ACTTGGTGGTGGTCCACAGCGTTTTCTGTGACAGTGCCATTTGCTTGACCTACCTCA 229
Db 365 ACCTCACCCCTGGCCACTTCCTGTCTCTACTACCGTACCGCTTCAGGATCTACTACTATG 424
QY 230 TCAAGAAGACTTTGGATGTTTTGGGCTGCCCTTCTCAAAATTTGTGAGTGCATGCTGCACA 289
Db 425 CTGCTGTTACTGATGTTTTGGGGAGATGCTGTGTAAGNGGTTCAGTGCATGATCCACG 484
QY 290 TCCATGATGATCTCAGCTTCTCTATTTCTATGTTGGTGTGCTGGTCCAGATACCTCATCT 349
Db 485 TGCATGATGATGCTTTTGTCTTCTACGTGGTTCATCTGCTGCTCATACGATGCTGGGGT 544
QY 350 TCTTCAAGTGCACAGACAAAGTGGAAATTTCTACAGAAACTGCATGCTGTGGCTGCCAGTG 409
Db 545 TCCATGACAGAGATGCTGCTACAGTTCTACAGAGAGTTCATGCTTTTGGCGCCAGTG 604
QY 410 CTGGCAGTGGACGCTGCTGATTTGTCATTTGTTGGTACCCCTGGTGTCTCCCGGTATGAA 469
Db 605 TGGCAGTGTGACAGTGTGCTTATGTTGTCATCCCCCCCCATCTCTTATTACAACTACGCA 664
QY 470 TCCATGAGGATACAA 485
Db 665 AGGACGTCCAGATAA 680

RESULT 13

CA965628 844 bp mRNA linear EST 03-JAN-2003
LOCUS CcLX05a15h17f1 Carp mixed tissue library 2 Cyprinus carpio cdna
DEFINITION clone 15h17 5', mRNA sequence.
ACCESSION CA965628
VERSION
KEYWORDS EST.
SOURCE Cyprinus carpio (common carp)
ORGANISM
Cyprinus carpio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE 1 (bases 1 to 844)
AUTHORS Gracey, A.Y., Fraser, E., Li, W. and Cossins, A.R.
TITLE Microarray and EST analysis of the carp (Cyprinus carpio) transcriptome during environmental stress
JOURNAL Unpublished (2003)
COMMENT Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 15 row: h column: 17
Seq primer: TripleX 5' LD (5'-CTGGGAAGCGCCCATGTGTGGT-3')
High quality sequence start: 39
High quality sequence stop: 580.
Location/Qualifiers
1. .844
/organism="Cyprinus carpio"
/mol_type="mRNA"
/db_xref="taxon:7962"
/clone="15h17"
/sex="Male & female"

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramatsu, K., Hiraoka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, K., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>

FEATURES

source

1. 2774
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A530099J19"
/db_xref="MGI:2406345"
/db_xref="taxon:10090"
/clone="A530099J19"
/sex="male"
/tissue_type="aorta and vein"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
311..1210
dev_stages="adult"

CDS

/note="unnamed protein product; hypothetical Rhodopsin-like GPCR superfamily containing protein (InterPro|IPR000276, evidence: InterPro) putative"

/codon_start=1
/protein_id="BAC30904.1"
/db_xref="GI:26334373"
/translation="MDVMDVLSNGSVMPMAEQVCDHCRALITAYSVVFFGT VGTVMHMFRRKQSMIATIIINIIHLISLLISLPRLSYFSAVKLGSPFCRM VGVYIGHMYLTFYVAIVLRLIYFKLQMOQLKQFHAVALSIITWTGSIIFLP IFPLQYGDPSYTSQRCFEFHSKLSNRDIIINYSIIVIMTTLILFLIQAVILH LKAYWDMWAHQRYRAIKSPFELLIVVCFIHPHAFRVYFIQNPPEQENSKLILN EICVALTAFCLDMELCTFGGVH"

ORIGIN

Query Match 15.9%; Score 146.2; DB 11; Length 2774;
Best Local Similarity 51.7%; Pred. No. 1.7e-28;
Matches 412; Conservative 0; Mismatches 373; Indels 12; Gaps 3;
QY 77 TAGCTTATTGGCGGCTGGTGGTGCATTCATTCATTCCTCTCTCTGTAATGA 136
DB 423 TGGTCTCTTTGGAGGACCGGTGGAAACAGTATGATGTCACATGATGTTCAAGAGGA 482
QY 137 ACACCCGCTAGTGACCAACCATGGCGGTCAATTAACCTGGTGGTGTCCACAGCGGTTTTC 196
DB 483 ATTGCCATCATGATTGCCACTATCATCATTAATCATTTGTTGGCACTCCCTTCTCC 542
QY 197 TGCTGACAGTGCCATTTCGCTTGACCTACCTCATCAAGAAGACTTGGATGTTGGGCTGC 256
DB 543 TGAATTAGTCTGCCATTCGCGCTCAGTTACTATTTCTCAGCAGTCTGGAAGCTTGGGTCT 602

QY 257 CCTCTCGAAAATTGTGAGTGCCATGCTGCGACATCCACATGCTACCTCAGTTCCTATTCT 316
DB 603 TTACCTCGCGAATGGTGTAGTGGCGTCATATATGGTCATATGTTACCTTACCTTCAITTTT 662
QY 317 ATGTGTGTATCTCTGTCACCATACCTCATCTTCTTCAAGTGCAGCAAGTGAAT 376
DB 663 ATGTGCGCAATGTTACCTCTCGCTGCTCATCTATTTTAAG--AACTGCAATGCAAC 719
QY 377 TCTACAGAAAATGATGCTGTGGCTGCCAGTGTGGCATGTGGACGCTGGTGTATGTCA 436
DB 720 AGTTACAAAAGTTCCATGCGCTGGCTCTAAGTATTTATTATTTGGGTGACAGGAAGCTTCA 779
QY 437 TTGTGTACCCCTGGTGTCTCCCGTATGGAATCCATGAGGAATACATGAGGAGCAC- 495
DB 780 TCTTTTACAAATATTTTTTTTACATATGGCACAGATCCAGTTATACAGAGCAACAGC 839
QY 496 --TGTTTTAAATTTCAAAAGAGCTGTGTTACATATGTGAAAATCATCAACTATATGA 553
DB 840 GGTGCTTTGAGTTTCATAAATCTCAACTCCAGGAGCATCATCATCAAAAATTTCTA 899
QY 554 TAGTCATTTTTCATAGCGGTGTGTCATCTGTGCTCTTCCAGGTCTTTCATCATTA 613
DB 900 TAAATGTTATATGATGACACAGTTCTGCTCTCTTCTGATACAGATGGCTGTCATTC 959
QY 614 TGTGTATGCTGCAGAGCTACGCCACTCTTTACTATCCACCAGAGTTCCTGGGCTCAGC 673
DB 960 TTCAATTTGATAAAGCCTATTGGCCCTATATGCGCCCATCAAGAGTACAGAGCTCAA 1019
QY 674 TGAATAACCTATTTTATAGGGTCACTCTGTTGTTGTTCTTCCCTACCACTGCTTTA 733
DB 1020 TCAAGAGTTTCTTCTCTGTTGTCATAGTTGTCTGCTTTTATACCCCACTGCAATTC 1079
QY 734 GGATCTATTACTTGAATGTTGACGCAATTCCAATGCCTGTAAACAGCAAGGTTGCAATTT 793
DB 1080 GGGTATATT-----TTATTCAAAATTTTCCAGAGCAAGAAATTTCTAAGTTAATTCTGT 1133
QY 794 ATAAAGAAATCTTCTTGAAGTGAACAGCAATTAAGTGTGATGCTATGCTCTCTTCTTGTCT 853
DB 1134 ACAATGAAATCTGTGTGCTTTAAACAGCTTCTGCTGCTGATATGTTATGTTTCATAG 1193
QY 854 TTGGGGGAGGCAATTCG 870
DB 1194 GTGGTGTATCCATAG 1210

RESULT 11

AJ455645 834 bp mRNA linear EST 22-APR-2002
AJ455645 riken1 Gallus gallus cDNA clone 6b4r1, mRNA sequence.

ACCESSION AJ455645
VERSION AJ455645.1 GI:20265741
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 834)
AUTHORS Buerstedde, J.M.
TITLE Gallus gallus bursal lymphocyte EST
JOURNAL Unpublished (2002)
COMMENT Contact: Buerstedde JM
Cellular Immunology

Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: <http://genetics.hpi.uni-hamburg.de/dt40est.html>.
Location/Qualifiers

FEATURES

source

1. 834
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="6b4r1"
/cell_type="bursal lymphocyte"

polylinker, Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGCTGTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. RNA provided by Dr. Betrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Patima Bonaldo."

ORIGIN

Query Match 16.5%; Score 151.4; DB 12; Length 478;
Best Local Similarity 81.7%; Pred. No. 3.1e-30;
Matches 187; Conservative 0; Mismatches 41; Indels 1; Gaps 1;
QY 690 TATAGGGGTCATCTGTTTGTCTTCCTCCCTACACAGGTTGCATTTTAAAGGAATCTCTT 809
DB 1 TATAGGTCATCATTTATTATTTGTTT-CTTCCCTACCACTTCTTCAGGATTTATTACTTGTA 59
QY 750 TGTGTGACCAATCCATCCCTGTACACAGGTTGCATTTTAAAGGAATCTCTT 809
DB 60 TGTGTGACCAATCCATCCAGAGCTGTAAACAAAGTTGCATTTTAAAGGAATCTCTT 119
QY 810 GAGTGTAAACGCAATAGCTGCTATGATTTGCTTCTTCTTTGCTTTGGGGGAAGCCATTG 869
DB 120 GAGCACAACGCCATCAGCTGCTGTGATTTGCTTTTGTCTTTGCTTTGGAGGAAGCCATTG 179
QY 870 GTTTACCAAGATTAATGGCTATGGAATGTTGTTTGTGCGCTAG 918
DB 180 GGTTAGCAAAAGATTGTCACATGTGGAATGCTCTTATGCCATTAG 228

RESULT 9

BG221739 283 bp mRNA linear EST 21-APR-2001
LOCUS BG221739
DEFINITION R641554 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG221739
VERSION BG221739.1 GI:13747760
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 283)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random

TITLE

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL

21227151

MEDLINE

11329013

PUBMED

Contact: Scott J. Cain

Athersys, Inc. Cleveland, OH 44115, USA

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@atersys.com

High quality sequence stop: 233.

Location/Qualifiers

FEATURES

1..283
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/notes="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 16.1%; Score 148; DB 12; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.1e-29;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCCAATACCTCCAGGAATCTCTTCGATCTATAGTGACACCCCACTTA 60

DB 136 ATGCTGGCCCAATACCTCCAGGAATCTCTTCGATCTATAGTGACACCCCACTTA 195

QY 61 ATCAGCCTTACTTCAATAGTCTTATTGGCGGGCTGGTGGTGTCAATTCATTCCTTTTC 120

DB 196 ATCAGCCTTACTTCAATAGTCTTATTGGCGGGCTGGTGGTGTCAATTCATTCCTTTTC 255

QY 121 CTCCTGGTGAATAATGACACCCCGTCAG 148

DB 256 CTCCTGGTGAATAATGACACCCCGTCAG 283

RESULT 10

AK041317

LOCUS

AK041317

DEFINITION

Mus musculus adult male aorta and vein cDNA, RIKEN full-length

enriched library, clone:A53009J19 product:hypothetical

Rhodopsin-like GPCR superfamily containing protein, full insert

sequence.

ACCESSION

AK041317

VERSION

AK041317.1 GI:26334372

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1

Carninci, P. and Hayashizaki, Y.

AUTHORS

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

PUBMED

10349636

REFERENCE

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

AUTHORS

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

PUBMED

11042159

REFERENCE

3

Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

AUTHORS

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

PUBMED

11076861

REFERENCE

4

The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2774)

```

/mcl_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match      20.6%; Score 189; DB 14; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGGACAAATACCTCCAGAAATCTCTTGGATCCTATAGTGACACCCACTTA 60
DB 311 ATGCTGGGACAAATACCTCCAGAAATCTCTTGGATCCTATAGTGACACCCACTTA 370
QY 61 ATCAGCTCTATCTATAGTCTTATTTGGGGCTGGTGGTGTCTATTTCCATTTTC 120
DB 371 ATCAGCTCTATCTATAGTCTTATTTGGGGCTGGTGGTGTCTATTTCCATTTTC 430
QY 121 CTCCTGGTGAATGAACCCCGTCAAGTACACCAATGCGGTCAATTAACCTGGTGG 180
DB 431 CTCCTGGTGAATGAACCCCGTCAAGTACACCAATGCGGTCAATTAACCTGGTGG 490
QY 181 GTCCACAGC 189
DB 491 GTCCACAGC 499

RESULT 7
BG461295
LOCUS
DEFINITION
RST44080 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION
BG461295
VERSION
BG461295.1 GI:13749801
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 649)
AUTHORS
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
Mays,R., Smith,B., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
TITLE
Activation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL
Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE
21227151
PUBMED
11329013
COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaine@atersys.com.
FEATURES
Location/Qualifiers
1..649
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/notes="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
Query Match      19.3%; Score 176.8; DB 12; Length 649;

```

```

Best Local Similarity 75.5%; Pred. No. 3.8e-37;
Matches 323; Conservative 0; Mismatches 47; Indels 58; Gaps 6;

QY 38 ATCTATAGTGACACCCACCTTAATACGCTCTACTTTCATAGTCTTATTGGCGGCTGG 97
DB 143 ATCTATAGTGACACCCACCTTAATACGCTCTACTTTCATAGAGCTTATTGGCGGCTGG 202
QY 98 TGGGTGTCATTTCCATTTCTTTCTCTCTGGTGAATAACACCCGGTCAAGTACACCA 157
DB 203 AGGGTGTCTATTTCCATTTCTTTCTCTCTGGTGAATAACACCCGGTCAAGTACACCA 245
QY 158 TGGCGGTCTATTAACCTGGTGTGTGCACACGCTTTTCTGTGCACAGTG-CCATTTTCG 216
DB 246 TGGCGGTCTATTAACCTGGTGTGTGCACACGCTTTTCTGTGCACAGTGCCCATTTTCG 305
QY 217 TTGACCTACCTCATCAAGAGACTTGGATGTTGGGTGCGCTTCTGCAAAATTTGTGAGT 276
DB 306 TTGACCTACC-----CTTTGGGTGCGCTTCTGCAAAATTTGTGAGT 347
QY 277 GCCATGTGCACATCCACATGTACCTCAGCTTCCT-ATTCTATGTGTGATCTCTGGTGCAC 335
DB 348 ACCATGCTCAACATTCATGTACCTGACGATCTTAATTTCTATGGCGTGTATCTCGCGCC 407
QY 336 CAGATACCTCATCTTCTTCAAGTGCAAGACAAAGTGGAAATTTACAGAAAACCTGCATGC 395
DB 408 CGGAT-----CAAGACAAAGCGACTT-TACAGAGTGTCTGGCCCC 446
QY 396 TGTGGCTGCCAGTCTGCGCATGTGGACGCTGGTGTGATTTGATGTGTGATCCCTGTGTGT 455
DB 447 CGAGGTGGCCAGAGCTGGCATGTGGACCTGTTGATTTGTATCTACGCGGCCCCCGCGTGT 506
QY 456 CTCGCCGT 463
DB 507 TTCGGGT 514

RESULT 8
BG145683
LOCUS
DEFINITION
mac33c07.Y1 Soares mouse 3Nm5 Mus musculus cDNA clone
IMAGE:4001652 5', mRNA sequence.
ACCESSION
BG145683
VERSION
BG145683.1 GI:12649019
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 478)
AUTHORS
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1499380
Seq primer: -40RP from Gibco
High quality sequence stop: 392.
FEATURES
Location/Qualifiers
1..478
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4001652"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified

```


end was generated during the Red process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACE3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. .684
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-007G22.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

FEATURES

source

ORIGIN

Query Match 59.0%; Score 542; DB 29; Length 684;
Best Local Similarity 98.2%; Pred. No. 3e-137;
Matches 548; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 361 AAGACAAAGTGAATCTACAGAAACTGCATGCTGCTGCCAGTCTGCCATGTGG 420
DB 10 AAAAAATCCGCGCTTCTACAGAAACTGCATGCTGCTGCCAGTCTGCCATGTGG 69
QY 421 ACCTCGTGAATTCATTTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480
DB 70 ACCTCGTGAATTCATTTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 129
QY 481 TACAATGAGAGACACTGTTTAAATTTCAAAAGACTGCTGTACACATATGTGAAATC 540
DB 130 TACAATGAGAGACACTGTTTAAATTTCAAAAGACTGCTGTACACATATGTGAAATC 189
QY 541 ATCAACTATATGATGATCAATTTTGTATAGCGGTTGCTGTGATTCGTGCTTCCAG 600
DB 190 ATCAACTATATGATGATCAATTTTGTATAGCGGTTGCTGTGATTCGTGCTTCCAG 249
QY 601 GCTTCATCATTAATGTTGATGTTGAGAGAGCTACGCCACTCTTTACTATCCACAGGAG 660
DB 250 GTCTTCATCATTAATGTTGATGTTGAGAGAGCTACGCCACTCTTTACTATCCACAGGAG 309
QY 661 TTCGGGCTCAGCTGAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCC 720
DB 310 TTCGGGCTCAGCTGAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCC 369
QY 721 TACCAGTCTTTAGGATCTATTACTTTGAATGTTGTGACGCAATCCCAATGCCGTGAACAGC 780
DB 370 TACCAGTCTTTAGGATCTATTACTTTGAATGTTGTGACGCAATCCCAATGCCGTGAACAGC 429
QY 781 AAGGTTGCATTTTATACGAAATCTTCTGAGTTAAGCAATAGCTGCTATGATTG 840
DB 430 AAGGTTGCATTTTATACGAAATCTTCTGAGTTAAGCAATAGCTGCTATGATTG 489
QY 841 CTTCCTCTTTGCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATATTTGGCTTATGGAAT 900
DB 490 CTTCCTCTTTGCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATATTTGGCTTATGGAAT 549
QY 901 TGTGTTTGTGCGGTTAG 918
DB 550 TGTGTTTGTGCGGTTAG 567

RESULT 2

BF160725

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

BF160725 772 bp mRNA linear EST 30-OCT-2000
601769127F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3988230 5',
mRNA sequence.
BF160725
BF160725.1 GI:11040832
EST.
Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 772)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Sequencing by: Incyte Genomics, Inc.

DNA Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9196 row: f column: 07

High quality sequence stop: 634.

Location/Qualifiers

1. .772

/organism="Mus musculus"

/mol_type="mRNA"

/strain="Czech II"

/db_xref="taxon:10090"

/clone="IMAGE:3988230"

/tissue_type="spontaneous tumor, metastatic to mammary."

Stem cell origin."

/lab_host="DH10B"

/clone_lib="NCI CGAP Lu29"

/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Salt;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 45.3%; Score 416.2; DB 10; Length 772;
Best Local Similarity 79.1%; Pred. No. 9.7e-103;
Matches 545; Conservative 0; Mismatches 138; Indels 6; Gaps 4;

QY 91 GGGCTGGTGGTGCATTTCCATTCCTCTCTCTGTAAGTGAACACCCGGTCAGTG 150

DB 1 GGACTGGTAGCCCTCATCTCCATCTCTTCTGCTGTAAGTGAACACTCACGTTCAAGT 60

QY 151 ACCACCATGGCGGTCAATTAACCTGGTGGTGCACACGCTTTCTCTGTCGACAGTCCCA 210

DB 61 ACCACCATGGTGTGCATCAACCTGGTGGTTCATGGGCTCTTCTACTGACGGTCCCT 120

QY 211 TTTGCTTGACCTACCTCATCAAGACAGCTTGAGATGTTGGGCTGCCCTTCTGCAAAATTT 270

DB 121 TTCGGCTTGGCATACCTCATCAAGGACCTTGGACG-TTGGATTTACCCCTTCTGCAAAATTT 179

QY 271 GTGAGTSCCATGCTGCACATCCATCTACTCAGCTTCTCTATCTATGTTGGTGCCTG 330

DB 180 GTGAGTSCCATGTTACATATCCATGTAATCTCATCTCTCTTCTACGTTGGTACTA 239

QY 331 GTCACAGATACCTCATCTTTCTTCAAGTGCACACAGACAAAGTGAATTTCTACAGAAATCTG 390

DB 240 GTCATCAGATACCTCATCTTTCTTCAAGTGCACACAGACAAAGTGAATTTCTACAGAAATCTG 299

QY 391 CATGCTGTGGCTGCAGTGGTGGCATCTGACGCTGGTGTGTCATGTTGTTGACCCCTG 450

DB 300 CATGAGTGTGTCGAAGTCTGCCATCTGGGCTTCTGGTGTGTTATTTGTTGCCCCCTG 359

QY 451 GTTGTCTCCCGGTATGGAATCCATGAGAAATACAATGAGGAGCAGCTGTTTAAATTTTAC 510

DB 360 GTGTTTCTCAGTATGGAATAGTGAAGATACAAATGAGCAACAGTCTTTAGATTCAT 419

QY 511 AAAGAGCTTGTACATATGTGAAATCATCACTATATGATGATGATGATGATGATGATGATGATG 570

DB 420 AAAGAGCTTGTGCAATGATTTCTGTGCGAGTTATCAACTACATGATGATGATGATGATGATGATG 479

QY 571 GCCGTTGCTGTGATTTCTGTTGGTCTTCCAGTCTTTCATCATTTATGTTGATGTTGTCAGAG 630

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 15:13:09 ; Search time 2947 Seconds
(without alignments)
9302.166 Million cell updates/sec

Title: US-10-055-106C-1

Perfect score: 918

Sequence: 1 atgctggccacaatacctc.....attgtgtttgtgcgcttag 918

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmvi:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	542	59.0	684	29	AG145972 Pan trogl
2	416.2	45.3	772	10	BF160725 601769127
3	351.4	38.3	580	28	AZ554824 RPCI-23-2
4	338	36.8	456	28	AQ888495 HS_3162_B

5	234.4	25.5	646	12	BG862323
6	189	20.6	499	14	CD699779
7	176.8	19.3	649	12	BG461295
8	151.4	16.5	478	12	BG145683
9	148	16.1	293	12	BG221739
10	146.2	15.9	2774	11	AK041317
11	142	15.5	834	9	AJ455645
12	111	12.1	680	14	CA355790
13	104.4	11.4	844	14	CA365628
14	83.6	9.1	661	13	BY748361
15	77.8	8.5	679	14	CD469227
16	72.2	7.9	733	13	CA050323
17	71.4	7.8	648	14	CB514350
18	70	7.6	659	13	BQ563030
19	70	7.6	986	29	AY401267
20	69.8	7.6	879	29	AY410745
21	69.4	7.6	866	14	CD246184
22	69.4	7.6	980	12	BM543468
23	64.4	7.0	671	13	BY752012
24	62.6	6.8	353	13	BY183952
25	61.2	6.7	679	13	BY750559
26	60.2	6.6	785	12	BI754749
27	60	6.5	450	14	CA576592
28	60	6.5	607	10	BB634972
29	60	6.5	689	13	BY751880
30	59.8	6.5	2919	11	AK038620
31	59.8	6.5	2959	11	AK079529
32	59	6.4	695	13	BY751732
33	58	6.3	791	14	CD559646
34	58	6.3	791	14	CD559647
35	58	6.3	792	14	CD559648
36	57.6	6.3	631	14	CB476420
37	57	6.2	895	14	CB565888
38	55.8	6.1	653	10	BB636445
39	55.6	6.1	730	14	CF147825
40	55.2	6.0	623	12	BQ038875
41	55.2	6.0	640	10	BE198338
42	55.2	6.0	1257	29	AY400333
43	54.2	5.9	654	10	AW373832
44	54	5.9	1257	29	AY400332
45	53.6	5.8	1393	12	BM546464

ALIGNMENTS

RESULT 1
AG145972
LOCUS AG145972 Pan troglodytes DNA, clone: RP43-007G22.TU, genomic survey
DEFINITION AG145972 Pan troglodytes DNA, clone: RP43-007G22.TU, genomic survey
ACCESSION AG145972.1 GI:16675650
VERSION AG145972.1
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.
TITLE BAC and sequences of Library RPCI-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 684)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC

Homo sapiens.
Key Location/Qualifiers
CD5 381..1400
/*tag= a
/product= "Human GCREC-6 protein"

WO200226825-A2.

04-APR-2002.

28-SEP-2001; 2001WO-US030661.

29-SEP-2000; 2000US-0235548P.

13-OCT-2000; 2000US-0240589P.

20-OCT-2000; 2000US-024223P.

20-OCT-2000; 2000US-0242322P.

03-NOV-2000; 2000US-0245855P.

03-NOV-2000; 2000US-0245900P.

09-NOV-2000; 2000US-0247587P.

15-NOV-2000; 2000US-0249343P.

(INCY-) INCYTE GENOMICS INC.

Baughn MR, Graul RC, Wallia NK, Gandhi AR, Hafalia AJA;

Ramkumar J, Tribouley CM, Thornton M, Kallick DA, Yao MG;

Elliott VS, Burford N, Khan PA, Yue H, Lu Y, Arvizu C, Roopa R;

Nguyen DB, Lee EA, Lu DAM, Ison CH, Walsh RT, Policky JL;

WPI; 2002-426012/45.

P-PSDB; AAE23414.

Novel G-protein coupled receptor polypeptides referred as GCREC peptides,

useful for treating multiple sclerosis, cholecystitis heart failure,

PT angina pectoris, rheumatoid arthritis, obesity, osteoporosis.

Claim 83; Page 140; 147pp; English.

The invention relates to human G-protein coupled receptor (GCREC 1-16)

polypeptides and polynucleotides. Sequences of the invention are useful

for the diagnosis, treatment and prevention of cell proliferative (e.g.

cancer, cirrhosis), neurological (e.g. multiple sclerosis, Huntington's

disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris,

heart failure), gastrointestinal (e.g. anorexia, cholecystitis),

autoimmune/inflammatory (rheumatoid arthritis, Hashimoto's thyroiditis)

and metabolic disorders (e.g. obesity, osteoporosis), viral infections,

atherosclerosis and hepatitis. GCREC proteins are useful for identifying

compounds that modulate mimic and block olfactory and taste sensations.

They are also useful for identifying GCREC modulators. GCREC DNAs are

useful in gene therapy. The present sequence is human GCREC-6 cDNA

Sequence 1499 BP; 375 A; 340 C; 329 G; 455 T; 0 U; 0 Other;

Query Match 97.5%; Score 895; DB 6; Length 1499;

Best Local Similarity 99.9%; Pred. No. 3e-254;

Mismatches 0; Conservative 0; Indels 1; Gaps 1;

OS	XX	1	ATGCTGGCCCAATACCTCCAGGAATTCCTCTTGGATCCCTATAGTGACACCCACCTTA	60
XX	DB	381	ATGCTGGCCCAATACCTCCAGGAATTCCTCTTGGATCCCTATAGTGACACCCACCTTA	440
XX	QY	61	ATCAGCCTCTACTCATAGTGCTTATTTGGCGGGCTGGTGGTGCATTTCCATTCTTTTC	120
XX	DB	441	ATCAGCCTCTACTCATAGTGCTTATTTGGCGGGCTGGTGGTGCATTTCCATTCTTTTC	500
XX	QY	121	CTCCTGGTGAATAAGAACCCGGTCAGTGACCAACCATGGCGGTCAATTAACCTGGTGGT	180
XX	DB	501	CTCCTGGTGAATAAGAACCCGGTCAGTGACCAACCATGGCGGTCAATTAACCTGGTGGT	560
XX	QY	181	GTCCACAGGCTTTTCTGTGACAGTGCCATTCGCTTACCTACTCATCAGAGACT	240
XX	DB	561	GTCCACAGGCTTTTCTGTGACAGTGCCATTCGCTTACCTACTCATCAGAGACT	620

QY	241	TGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC	300
DB	621	TGATGTTGGGCTGCCCTTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC	580
QY	301	CTCAGCTTCCTATTCTATGTTGGTATCCTGGTACCAGATACCTCATCTCTTCAAGTGC	360
DB	681	CTCAGCTTCCTATTCTATGTTGGTATCCTGGTACCAGATACCTCATCTCTTCAAGTGC	740
QY	361	AAAGACAAAGTGAATTCACAGAAACCTGCATGCTGGCTGCCAGTCTGGCATGTGG	420
DB	741	AAAGACAAAGTGAATTCACAGAAACCTGCATGCTGGCTGCCAGTCTGGCATGTGG	800
QY	421	ACGCTGGTATTCCTCATTTGGTATCCCTCGGTATGGAATCCATGAGGAA	480
DB	801	ACGCTGGTATTCCTCATTTGGTATCCCTCGGTATGGAATCCATGAGGAA	860
QY	481	TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTCTACATATGTGAAATC	540
DB	861	TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTCTACATATGTGAAATC	920
QY	541	ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATTTCTTGGTCTTCCAG	600
DB	921	ATCAACTATATGATAGTCAATTTTGTATAGCCGTTGCTGTGATTTCTTGGTCTTCCAG	980
QY	601	GTCTTCATCATTTATGTTGATGTTGAGAGCTACGCCACTCTTTTACTATCCACAGGAG	660
DB	981	GTCTTCATCATTTATGTTGATGTTGAGAGCTACGCCACTCTTTTACTATCCACAGGAG	1040
QY	661	TTCTGGGCTCAGCTGAAACACCTATTTTATAGGGGTGATCCTCTGTTGTTTCTTCCC	720
DB	1041	TTCTGGGCTCAGCTGAAACACCTATTTTATAGGGGTGATCCTCTGTTGTTTCTTCCC	1100
QY	721	TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTTAAACAGC	780
DB	1101	TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCCAATGCTTAAACAGC	1160
QY	781	AAGTTGCATTTTATAACGAAATCTTCTGAGTGTACAGCAATTAGCTGCTATGATTG	840
DB	1161	AAGTTGCATTTTATAACGAAATCTTCTGAGTGTACAGCAATTAGCTGCTATGATTG	1220
QY	841	CTTCTCTTTCTCTTTGGGGAGCCATTTGCTTTAAGCAAAAGATAATTTGGCTTATGGAAT	900
DB	1221	CTTCTCTTTCTCTTTGGGGAGCCATTTGCTTTAAGCAAAAGATAATTTGGCTTATGGAAT	1279
QY	901	TGTGTTT 907	
DB	1280	TGTGTTT 1286	

Search completed: April 25, 2004, 15:49:32
Job time : 455 secs

```

FT CDS      1..939
FT          /tag= a
FT          /partial
FT          /product= "Human G-protein coupled receptor type protein
FT          93870"
FT          /note= "No stop codon"
FT
XX
FN MO200270657-A2.
XX
PD 12-SEP-2002.
XX
PF 28-FEB-2002; 2002WO-US006455.
XX
PR 01-MAR-2001; 2001US-0272677P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA;
XX
DR WPI: 2002-732793/79.
DR P-PSDB; AAO22919.
XX
XX New G-protein coupled receptor used in receptor assays as a target for
PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and
PT inflammatory disorders, platelet disorders, skeletal or bone metabolism
PT disorders.
XX
PS Claim 5; Page 101-103; 105pp; English.
XX
XX The invention relates to an isolated polypeptide, which is a G-protein
CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled
CC receptor type proteins (GPCRs), designated the 93870 receptor. The
CC polypeptides, nucleic acid molecules and antibodies of the invention are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC monitoring clinical trials or pharmacogenetics), or in methods of
CC treatment (e.g. therapeutic and prophylactic). They are useful in
CC treating and diagnosing conditions related to aberrant activity or
CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and
CC inflammatory disorders, platelet disorders, skeletal or bone metabolism
CC disorders, or bone marrow mononuclear disorders, as well as cellular
CC proliferative and/or differentiative disorders, hormonal disorders, liver
CC neurological disorders, cardiovascular disorders, viral diseases, liver
CC disorders, and pain and metabolic disorders. Conditions that can be
CC treated include cancer, diabetes mellitus, hypothyroidism, bacterial or
CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or
CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,
CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,
CC Huntington's disease, heart failure, angina pectoris, myocardial
CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,
CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host
CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The
CC transgenic animals are useful for studying the function and/or activity
CC of a 93870 protein and for identifying and/or evaluating modulators of
CC 93870 activities. The polynucleotides of the invention can be used in
CC gene therapy. This polynucleotide sequence represents the 939 nucleotide
CC DNA of the human G-protein coupled receptor type protein of the invention
XX
SQ Sequence 939 BP; 215 A; 212 C; 205 G; 307 T; 0 U; 0 Other;

```

```

Query Match      99.5%; Score 913.4; DB 6; Length 939;
Best Local Similarity 99.9%; Pred. No. 8.1e-260;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 ATGCTGGCCACATACCTCCAGGAATCTCTTGGCATCTATAGTACACCCACTTA 60
DB 25 ATGCTGGCCACATACCTCCAGGAATCTCTTGGCATCTATAGTACACCCACTTA 84
QY 61 ATCAGCCTCTACTTCATAGTCTTTATTGGGGGCTGGTGGTGCATTTTCATCTTTTC 120
DB 85 ATCAGCCTCTACTTCATAGTCTTTATTGGGGGCTGGTGGTGCATTTTCATCTTTTC 144
QY 121 CTCTGTGTAATGACACCCGGTCTAGTGACACCATCGGGTCATTACTTGGTGGTG 180

```

```

DB 145 CTCCTGGTGAATAATGAACACCCCGTCAGTGACCACCATCGCGGTCAATTAACTTGGTGGT 204
QY 181 GTCCACAGAGCTTTTCTGCTGACAGTCCGCTTTCGCTTACCTTACCTCATCAAGAGACT 240
DB 205 GTCCACAGAGCTTTTCTGCTGACAGTCCGCTTTCGCTTACCTTACCTCATCAAGAGACT 264
QY 241 TGGATGTTTGGGCTGCCCTTCTCAAAATTTGAGTGGCAATGTGCACATCCATGTATC 300
DB 265 TGGATGTTTGGGCTGCCCTTCTCAAAATTTGAGTGGCAATGTGCACATCCATGTATC 324
QY 301 CTCAGTTTCTATCTATGTTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 360
DB 325 CTCAGTTTCTATCTATGTTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 384
QY 361 AAAGACAAAGTGAATTTCTACAGAAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 385 AAAGACAAAGTGAATTTCTACAGAAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 444
QY 421 ACGTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 480
DB 445 ACGTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 504
QY 481 TACATGAGGAGCACTGCTTTTAAATTTTCAAAAGAGCTTCTTACACATATGTGAAAATC 540
DB 505 TACATGAGGAGCACTGCTTTTAAATTTTCAAAAGAGCTTCTTACACATATGTGAAAATC 564
QY 541 ATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 565 ATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 624
QY 601 GTCTTCATCATTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 660
DB 625 GTCTTCATCATTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 684
QY 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTGCATCTCTGTTGTTGTTGTTGTTGTTGTTGTT 720
DB 685 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTGCATCTCTGTTGTTGTTGTTGTTGTTGTTGTT 744
QY 721 TACCAAGTTCTTACGATCTATCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 780
DB 745 TACCAAGTTCTTACGATCTATCTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 804
QY 781 AAGTTTGCATTTTATACGAAATCTTCTTGTAGTGTAAACAGCAATAGTGTGTATGATTTG 840
DB 805 AAGTTTGCATTTTATACGAAATCTTCTTGTAGTGTAAACAGCAATAGTGTGTATGATTTG 864
QY 841 CTCTCTTTGCTTTGGGGGAGGCAATGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 900
DB 865 CTCTCTTTGCTTTGGGGGAGGCAATGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 924
QY 901 TGTGTTTGTGCGGT 915
DB 925 TGTGTTTGTGCGGT 939

```

RESULT 15
AAD37670

ID AAD37670 standard; cDNA; 1499 BP.

XX AAD37670;

XX 27-AUG-2002 (first entry)

XX Human G-protein coupled receptor-6 (GCR6-6) cDNA.

XX Human; G-protein coupled receptor-6; GCR6-6; atherosclerosis; cancer;
 XX cell proliferative disorder; gastrointestinal; autoimmune; metabolic;
 XX neurological; inflammatory; cardiovascular; viral infection; anorexia;
 XX cirrhosis; multiple sclerosis; Huntington's disease; gene therapy;
 XX Alzheimer's disease; heart failure; hepatitis; cholecystitis; obesity;
 XX rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris;
 XX osteoporosis; gene; ss.

XX Glucksmann MA;
XX WPI: 2002-732793/79.
DR P-PSDB; AAO22919.
XX
PT New G-protein coupled receptor used in receptor assays as a target for
PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and
PT inflammatory disorders, platelet disorders, skeletal or bone metabolism
PT disorders.
XX
PS Claim 5; Page 99-100; 105pp; English.
XX
CC The invention relates to an isolated polypeptide, which is a G-protein
CC coupled receptor (GPCR) related to Subfamily I of G-protein coupled
CC receptor type proteins (GPCRs), designated the 93870 receptor. The
CC polypeptides, nucleic acid molecules and antibodies of the invention are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC monitoring clinical trials or pharmacogenetics), or in methods of
CC treating (e.g. therapeutic and prophylactic). They are useful in
CC treating and diagnosing conditions related to aberrant activity or
CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and
CC inflammatory disorders, platelet disorders, skeletal or bone metabolism
CC disorders, or bone marrow mononuclear disorders, as well as cellular
CC proliferative and/or differentiative disorders, hormonal disorders, liver
CC neurological disorders, cardiovascular disorders, viral diseases, liver
CC disorders, and pain and metabolic disorders. Conditions that can be
CC treated include cancer, diabetes mellitus, hypothyroidism,
CC hyperthyroidism, fungal meningococcalitis, multiple sclerosis,
CC viral meningitis, Parkinson's disease, ataxia-telangiectasia,
CC Alzheimer's disease, heart failure, angina pectoris, myocardial
CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,
CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host
CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The
CC transgenic animals are useful for studying the function and/or activity
CC of a 93870 protein and for identifying and/or evaluating modulators of
CC 93870 activities. The polynucleotides of the invention can be used in
CC gene therapy. This polynucleotide sequence represents the cDNA of the
CC 1684 nucleotide human G-protein coupled receptor type protein of the
CC invention
XX
SQ Sequence 1684 BP; 435 A; 366 C; 351 G; 531 T; 0 U; 1 Other;
Query Match 99.8%; Score 916.4; DB 6; Length 1684;
Best Local Similarity 99.9%; Pred. No. 1.4e-260;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCTGGCCCAATACCTCCAGGAATTCCTTTGGATCCCTATAGTGACACCCCACTTA 60
DB 171 ATGCTGGCCCAATACCTCCAGGAATTCCTTTGGATCCCTATAGTGACACCCCACTTA 230
QY 61 ATCAGCCTTACTTCATAGTGCTTATGGCGGCTGGTGGGTGCTATTTCCATCTTTTC 120
DB 231 ATCAGCCTTACTTCATAGTGCTTATGGCGGCTGGTGGGTGCTATTTCCATCTTTTC 290
QY 121 CTCCTGGTGAATAAACAACCCGGTCAGTGACACCACTGGCGGTCAATTAACCTGGTGTG 180
DB 291 CTCCTGGTGAATAAACAACCCGGTCAGTGACACCACTGGCGGTCAATTAACCTGGTGTG 350
QY 181 GTCCACAGGTTTTCTGCTGACAGTGCATTCCTGCTGACCTACTCATCAGAGACT 240
DB 351 GTCCACAGGTTTTCTGCTGACAGTGCATTCCTGCTGACCTACTCATCAGAGACT 410
QY 241 TGGATGTTGGGCTGCCCTTCGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300
DB 411 TGGATGTTGGGCTGCCCTTCGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 470
QY 301 CTCAGCTTCCTATTCATAGTGCTGATTCCTGGTGCACAGATCCTCATCTTCTCAAGTGC 360
DB 471 CTCAGCTTCCTATTCATAGTGCTGATTCCTGGTGCACAGATCCTCATCTTCTCAAGTGC 530
QY 361 AAAGACAAAGTGAATTCCTACAGAAATCTGCTGCTGGCTGCCAGTGGCTGGCATGTGG 420

DB 531 AAAGACAAAGTGAATTCCTACAGAAATCTGCTGCTGGCTGCCAGTGGCTGGCATGTGG 590
QY 421 ACCTGGTGTATTCATTTGGTGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480
DB 591 ACCTGGTGTATTCATTTGGTGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA 650
QY 481 TACAATGAGGAGACCTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAAATC 540
DB 651 TACAATGAGGAGACCTGTTTAAATTTCAAAAGAGCTTGTACACATATGTGAAATC 710
QY 541 ATCAACTATATGATGATGATTTTGTATGACGCGTGTGTGATTCCTGTTGGTCTTCCAG 600
DB 711 ATCAACTATATGATGATGATTTTGTATGACGCGTGTGTGATTCCTGTTGGTCTTCCAG 770
QY 601 GTCTTCATCATTTATGTTGATGTCGAGAACTACGCCACTTTTATATATCCACAGGAG 660
DB 771 GTCTTCATCATTTATGTTGATGTCGAGAACTACGCCACTTTTATATATCCACAGGAG 830
QY 661 TTCTGGGCTCAGCTGAAAACCTATTTTATATAGGGGTGATCCTGTTGTTTCCCTCCC 720
DB 831 TTCTGGGCTCAGCTGAAAACCTATTTTATATAGGGGTGATCCTGTTGTTTCCCTCCC 890
QY 721 TACCAGTTCCTTTAGGATCTATTACTTTGAATGTTGTGACGCAATCCATGCTGTAAACAGC 780
DB 891 TACCAGTTCCTTTAGGATCTATTACTTTGAATGTTGTGACGCAATCCATGCTGTAGCAGC 950
QY 781 AAGTTGCATTTTATACGAAATCTTCTTCTGAGTGTAACAGCAATAGCTGCTATGATTG 840
DB 951 AAGTTGCATTTTATACGAAATCTTCTTCTGAGTGTAACAGCAATAGCTGCTATGATTG 1010
QY 841 CTCTCTCTTCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
DB 1011 CTCTCTCTTCTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 1070
QY 901 TGTGTTTGTGCGCTTAG 918
DB 1071 TGTGTTTGTGCGCTTAG 1088
RESULT 14
AAL53414
ID AAL53414 standard; DNA; 939 BP.
XX
AC AAL53414;
XX
DT 12-DEC-2002 (first entry)
DE
XX 939 nt coding DNA of a human G-protein coupled receptor type protein.
KW Anti-HIV; cytostatic; antidiabetic; antiaesthetic; antiinflammatory;
KW haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;
KW antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;
KW cardiant; dermatological; antifertility; hepatotropic; antiallergic;
KW antipsoriatic; ophthalmological; antiangiinal; antithyroid; anticonvulsant;
KW antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;
KW 93870 receptor; immune; inflammatory disorder; platelet disorder;
KW skeletal; bone metabolism disorder; bone marrow mononuclear disorder;
KW cellular proliferative; differentiative disorder; hormonal disorder;
KW neurological disorder; cardiovascular disorder; viral disease; pain;
KW liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;
KW hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;
KW viral meningitis; fungal meningococcalitis; multiple sclerosis;
KW Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;
KW Huntington's disease; heart failure; angina pectoris; dermatitis;
KW myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;
KW inflammatory bowel disease; asthma; graft-versus-host disease; allergy;
KW conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;
KW transgenic animal; human; gene; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH

XX PS Claim 1; Page 6; 58pp; English.

XX CC The invention relates to a G protein-coupled receptor (GPCR) IGS70

XX CC polypeptide including sequences that are 98-99.6% identical. Also

XX CC included are the polynucleotide encoding IGS70 (including sequences 98-

XX CC 99.6% identical to the polynucleotide or the DNA insert contained in

XX CC plasmid CBS 109818), a hybridisation probe derived from the

XX CC polynucleotide, a DNA or RNA expression system producing IGS70, a host

XX CC comprising the expression system, IGS70 receptor membrane preparation

XX CC derived from the cell, an antibody immunospecific for IGS70, IGS70 is

XX CC useful for diagnosing a disease or a susceptibility to disease in a

XX CC subject related to expression or activity of the IGS70 polypeptide in a

XX CC subject by determining the presence or absence of mutation in the

XX CC nucleotide sequence encoding IGS70 in the genome of the subject in a

XX CC sample derived from the subject. IGS70 is also useful identifying agonist

XX CC or antagonist. The IGS70 protein, polynucleotide, antibody and identified

XX CC ant/agonists are useful for treating psychiatric and central nervous

XX CC system (CNS) disorders such as schizophrenia, Alzheimer's disease,

XX CC multiple sclerosis, anxiety, cardiovascular diseases such as heart

XX CC failure, angina pectoris, myocardial infarction, kidney disease such as

XX CC renal failure, gastrointestinal disorders such as irritable bowel

XX CC syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,

XX CC inflammation, cancers, asthma, infection (such as bacterial, viral,

XX CC fungal, protozoal) especially human immunodeficiency virus infection

XX CC (HIV), diabetes, osteoporosis and allergies. The present sequence encodes

XX CC the human GPCR IGS70

SQ Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other;

Query Match 99.8%; Score 916.4; DB 6; Length 1051;

Best Local Similarity 99.9%; Pred. No. 1.1e-260;

Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGCATCTCTATAGTGACACCCCACTTA 60

DB 60 ATGCTGGCCACAAATACCTCCAGAAATCTCTTGGCATCTCTATAGTGACACCCCACTTA 119

QY 61 ATCAGCTCTACTCTAGTGTCTATTGGGGCTGGTGGTCTCATTTCCATCTTTTC 120

DB 120 ATCAGCTCTACTCTAGTGTCTATTGGGGCTGGTGGTCTCATTTCCATCTTTTC 179

QY 121 CTCCTGGTGAATAATGAACCCCGTCAAGTACCAACCATGCGGTCTTAATCTGGTGGTG 180

DB 180 CTCCTGGTGAATAATGAACCCCGTCAAGTACCAACCATGCGGTCTTAATCTGGTGGTG 239

QY 181 GTCCACAGGTTTTCTGTGACAGTGCATTTTCGTTGACCTACCTCATCAAGAGACT 240

DB 240 GTCCACAGGTTTTCTGTGACAGTGCATTTTCGTTGACCTACCTCATCAAGAGACT 299

QY 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGTCACATCCACATGTAC 300

DB 300 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGTCACATCCACATGTAC 359

QY 301 CTCAGGTTCTTATCTATGTGGTGATCTGGTCCACAGATACCTCATCTTCTCAAGTGC 360

DB 360 CTCAGGTTCTTATCTATGTGGTGATCTGGTCCACAGATACCTCATCTTCTCAAGTGC 419

QY 361 AAAGACAAAGTGGAAATCTTACAGAAATCTGATGTTGCTGCCAGTCTGCGATGGG 420

DB 420 AAAGACAAAGTGGAAATCTTACAGAAATCTGATGTTGCTGCCAGTCTGCGATGGG 479

QY 421 ACCTGGTATGTCATTTGGTGTACCCCTGGTGTCTCCCGGATCGAATCCATGAGGAA 480

DB 480 ACCTGGTATGTCATTTGGTGTACCCCTGGTGTCTCCCGGATCGAATCCATGAGGAA 539

QY 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAGAGCTTGGCTTACACATATGTGAATTC 540

DB 540 TACAATGAGGAGCAGCTGTTTAAATTTCAAGAGCTTGGCTTACACATATGTGAATTC 599

QY 541 ATCAACTATATGATGATCAATTTTGTATGACCGGTTGCTGTGATCTGTGGTCTCCAG 600

DB 600 ATCAACTATATGATGATCAATTTTGTATGACCGGTTGCTGTGATCTGTGGTCTCCAG 659

QY 601 GTCTTCATCATTTATGTTGATGGTGCAGAGCTAGCCCACTCTTTTACTATCCCAAGAG 660

DB 660 GTCTTCATCATTTATGTTGATGGTGCAGAGCTAGCCCACTCTTTTACTATCCCAAGAG 719

QY 661 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTCACTCTTGTGTTTCTTCCC 720

DB 720 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGGTCACTCTTGTGTTTCTTCCC 779

QY 721 TACCAGTTCTTTAGGATCTATTACTTGAATCTTGTGACGCAATTCCTCAATGCTGTAACAGC 780

DB 780 TACCAGTTCTTTAGGATCTATTACTTGAATCTTGTGACGCAATTCCTCAATGCTGTAACAGC 839

QY 781 AAGTTGTCATTTTAAACGAAATCTTCTTGTAGTGTAAACAGCAATTAGCTGATGTTG 840

DB 840 AAGTTGTCATTTTAAACGAAATCTTCTTGTAGTGTAAACAGCAATTAGCTGATGTTG 899

QY 841 CTCTCTCTTGTCTTGGGGGAGCCATGTTTAAAGCAAAAGATAAATGGCTTATGAAT 900

DB 900 CTCTCTCTTGTCTTGGGGGAGCCATGTTTAAAGCAAAAGATAAATGGCTTATGAAT 959

QY 901 TGTGTTTGTCCCGTTAG 918

DB 960 TGTGTTTGTCCCGTTAG 977

RESULT 13

AAL53413

ID AAL53413 standard; cDNA; 1684 BP.

XX AC AAL53413;

XX AC AAL53413;

DT 12-DEC-2002 (first entry)

XX DE 1684 nt cDNA of human G-protein coupled receptor type protein.

XX KW Anti-HIV; cytostatic; antidiabetic; antiasthmatic; antiinflammatory;

XX KW haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;

XX KW antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;

XX KW cardiant; dermatological; antiinfertility; hepatotropic; antiallergic;

XX KW antiporiatic; ophthalmologic; antiangular; antithyroid; anticonvulsant;

XX KW anirhematic; antiarthritic; G-protein coupled receptor; subfamily 1;

XX KW 93870 receptor; immune; inflammatory disorder; bone marrow mononuclear disorder;

XX KW skeletal; bone metabolism disorder; bone marrow mononuclear disorder;

XX KW cellular proliferative; differentiative disorder; hormonal disorder;

XX KW neurological disorder; cardiovascular disorder; viral disease; pain;

XX KW liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;

XX KW hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;

XX KW viral meningitis; fungal meningoencephalitis; multiple sclerosis;

XX KW Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;

XX KW Huntington's disease; heart failure; angina pectoris; dermatitis;

XX KW myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;

XX KW inflammatory bowel disease; asthma; graft-versus-host disease; allergy;

XX KW conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;

XX KW transgenic animal; human; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 147..1088

XX FT /*tag= a

XX FT /product= "Human G-protein coupled receptor type protein

XX FT 93870"

XX PN WO200270657-A2.

XX PD 12-SEP-2002.

XX XX 28-FEB-2002; 2002WO-US006455.

XX PF 01-MAR-2001; 2001US-0272677P.

XX PR (MILL-) MILLENNIUM PHARM INC.

XX PA

XX 02-JAN-2003.
 XX PD
 XX PF
 XX 18-JUN-2002; 2002EP-00013517.
 XX PR
 XX 18-JUN-2001; 2001JP-00246789.
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX Suwa M, Asai K, Akiyama Y, Aburatani H;
 XX WPI; 2003-315783/31.
 DR P-PSDB; ADC86555.
 XX
 PT New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.
 XX
 PS Claim 1; SEQ ID NO 1007; 28pp; English.
 XX
 CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The
 CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
 CC invention.
 XX
 SQ Sequence 113306 BP; 34476 A; 21483 C; 21391 G; 35956 T; 0 U; 0 Other;
 Query Match 100.0%; Score 918; DB 9; Length 113306;
 Best Local Similarity 100.0%; Pred. No. 4.5e-260;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCTGTGCGCAATACCTCAGGAATTCCTTGGCATCTATAGTGACACCCCACTTA 60
 DB 11540 ATGCTGTGCGCAATACCTCAGGAATTCCTTGGCATCTATAGTGACACCCCACTTA 11599
 QY 61 ATCAGCCTCTACTCATAGTGTCTATTGGCGGGTGGTGGTGCATTTTCATTCTTTTC 120
 DB 11600 ATCAGCCTCTACTCATAGTGTCTATTGGCGGGTGGTGGTGCATTTTCATTCTTTTC 11659
 QY 121 CTCCTGTGTGAATGAACACCCGGTCACTGACACCACTGGCGGTCAATTAACCTTGGTGTG 180
 DB 11660 CTCCTGTGTGAATGAACACCCGGTCACTGACACCACTGGCGGTCAATTAACCTTGGTGTG 11719
 QY 181 GTCCACAGCGTTTTCTGCTGACAGTGCATTTGCTTGACCTACCTCATCAAGAAGACT 240
 DB 11720 GTCCACAGCGTTTTCTGCTGACAGTGCATTTGCTTGACCTACCTCATCAAGAAGACT 11779
 QY 241 TGGATGTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCATGTAC 300
 DB 11780 TGGATGTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCATGTAC 11839
 QY 301 CTCAGTTCTTATCTATGTGGTGAATCTGTGTCACCAAGATACCTCATCTTCTTCAAGTGC 360
 DB 11840 CTCAGTTCTTATCTATGTGGTGAATCTGTGTCACCAAGATACCTCATCTTCTTCAAGTGC 11899
 QY 361 AAGACAAAGTGGAAATCTCAGAAATCTGATGCTGGCTGCAGTGGCGATGG 420
 DB 11900 AAGACAAAGTGGAAATCTCAGAAATCTGATGCTGGCTGCAGTGGCGATGG 11959
 QY 421 ACGTGTGTATGTGATTTGATGCTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480
 DB 11960 ACGTGTGTATGTGATTTGATGCTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 12019
 QY 481 TACATGAGGACACTGTTTAAATTTTCAAAAGCTTGTCTACATATGTGAAATC 540
 DB 12020 TACATGAGGACACTGTTTAAATTTTCAAAAGCTTGTCTACATATGTGAAATC 12079
 QY 541 ATCAACTATATAGTAGTCATTTTGTGATAGCCGCTGTGCTGTGATTCCTTGGTCTTCCAG 600

DB 12080 ATCAACTATATAGTAGTCATTTTGTGATAGCCGTTGCTGTGATTCCTTGTGCTTCCAG 12139
 QY 601 GTCTTCATCATTTATGTTGATGGTGCAAGAGCTACGCCACTCTTTTACTATCCACACAGGAG 660
 DB 12140 GTCTTCATCATTTATGTTGATGGTGCAAGAGCTACGCCACTCTTTTACTATCCACACAGGAG 12199
 QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATATAGGGGTCACTCTTGTGTTTCTTCCCTCC 720
 DB 12200 TTCTGGGCTCAGCTGAAAAACCTATTTTATATAGGGGTCACTCTTGTGTTTCTTCCCTCC 12259
 QY 721 TACAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGCATTCCTCAATGCCGTGTACAGC 780
 DB 12260 TACAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGCATTCCTCAATGCCGTGTACAGC 12319
 QY 781 AAGGTTGCAATTTTATAACGAAATCTTCTTGAAGTGAACAGCAATTAGCTGTATGATTG 840
 DB 12320 AAGGTTGCAATTTTATAACGAAATCTTCTTGAAGTGAACAGCAATTAGCTGTATGATTG 12379
 QY 841 CTCTCTCTTGTCTTCTGGGGGAAGCCATTTGGTTTAACCAAAAGATTAATTCCTTAAGAT 900
 DB 12380 CTCTCTCTTGTCTTCTGGGGGAAGCCATTTGGTTTAACCAAAAGATTAATTCCTTAAGAT 12439
 QY 901 TGTGTTTGTGCGCGTTAG 918
 DB 12440 TGTGTTTGTGCGCGTTAG 12457
 RESULT 12
 ABK87351
 ID ABK87351 standard; cDNA; 1051 BP.
 XX
 AC ABK87351;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Human cDNA encoding G protein-coupled receptor IGS70.
 XX
 KW Human; ss; gene; G protein-coupled receptor; GPCR; IGS70; CNS;
 KW psychiatric disorder; central nervous system disorder; schizophrenia;
 KW Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;
 KW heart failure; angina pectoris; myocardial infarction; kidney disease;
 KW renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;
 KW inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;
 KW asthma; infection; human immunodeficiency virus infection; HIV; diabetes;
 KW osteoporosis; allergy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 60..977
 FT /*tag= a
 FT /product= "GPCR IGS70"
 XX
 PN WO200244212-A2.
 XX
 PD 06-JUN-2002.
 XX
 PF 23-NOV-2001; 2001WO-BP013706.
 XX
 PR 30-NOV-2000; 2000EP-00204280.
 PR 03-DEC-2000; 2000US-0251045P.
 XX
 PA (SOLV) SOLVAY PHARM BV.
 XX
 PI Deleersnijder W, Blockx H, De Moor L;
 XX WPI; 2002-527703/56.
 DR P-PSDB; AAU99179.
 XX
 PT Novel G-protein coupled receptor IGS70 polypeptide useful for treating
 PT dysfunctions, disorders or disease related to lung, bone marrow, spinal
 PT cord immune system.

XX Human; gene; ds; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
 KW nG protein coupled receptor; communication; serpentine structure;
 KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;
 KW genetic predisposition; brain; immune response; gene therapy;
 KW anxiety disorder; depression; bipolar disorder; schizophrenia;
 KW Huntington's disease; Alzheimer's disease; manic depression; stroke;
 KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
 KW tranquilizer.
 XX Homo sapiens.
 XX W0200264789-A1.
 XX 22-AUG-2002.
 XX 14-FEB-2001; 2001WO-US004641.
 XX 14-FEB-2001; 2001WO-US004641.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Lind P, Parodi LA, Vogeli G, Wood LS;
 XX WPI; 2002-674879/72.
 XX P-PSDB; ABG93787.
 XX New nucleic acids and polypeptides of the nG protein-coupled receptor,
 PT useful for treating or diagnosing a mental disorder or a disorder
 PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
 PT Parkinson's disease.
 XX Example 1; Page 84-85; 244pp; English.
 CC The invention discloses an isolated human polypeptide, and encoding
 CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
 CC nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
 CC communication between cells and their environment and are characterised
 CC by a serpentine structure that passes through the cell membrane seven
 CC times, hence the reason such receptors are sometimes called seven
 CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
 CC useful for identifying an nGPCR allelic variant that correlates with a
 CC mental disorder, for isolating an antibody that binds to an epitope of
 CC the polypeptide, and for identifying a compound that binds the polypeptide or
 CC polynucleotide and/or modulates its biological activity, for screening a
 CC human subject to diagnose a disorder, or a genetic predisposition to a
 CC disorder, affecting the brain or a genetic disposition to the disorder,
 CC for identifying compounds useful for the treatment of a mental disorder
 CC and for identifying a compound useful as a modulator of binding between
 CC nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also
 CC useful for inducing an immune response in a mammal. The nucleic acid or
 CC polypeptide is particularly useful, using gene therapy, for treating e.g.
 CC anxiety disorders, depression, bipolar disorder, schizophrenia,
 CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
 CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
 CC be used for treating diabetes, inflammation or wounds. The sequences
 CC presented in AB570202-AB570248, AB570338 and AB570243 are the DNAs
 CC encoding the nGPCRs (also referred to as beGPCRs)
 XX
 SQ Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;
 Query Match 100.0%; Score 918; DB 6; Length 2525;
 Best Local Similarity 100.0%; Pred. No. 6e-261;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ATGCGTGGCACAAATACCTCCAGAAATCTCTTGGGATCCTATAGTACACCCCACTTA 60
 27 ATGCGTGGCACAAATACCTCCAGAAATCTCTTGGGATCCTATAGTACACCCCACTTA 86
 61 ATGAGCCTCTACTTTCATAGTGGCTTATTGGGGGCTGGTGGTCTCATTTCTTCTTTC 120
 87 ATGAGCCTCTACTTTCATAGTGGCTTATTGGGGGCTGGTGGTCTCATTTCTTCTTTC 146

QY 121 CTCCTGGTGAATAAGAACACCCGGTCAGTGACCAACCATGCGGTCATTAACTTGGTGGT 180
 DB 147 CTCCTGGTGAATAAGAACACCCGGTCAGTGACCAACCATGCGGTCATTAACTTGGTGGT 206
 QY 181 GTCACACAGGTTTTCTCTGCTGACAGTGCATTTGGCTTGACCTACCTCATCAAGAAGACT 240
 DB 207 GTCACACAGGTTTTCTCTGCTGACAGTGCATTTGGCTTGACCTACCTCATCAAGAAGACT 266
 QY 241 TGGATGTTTGGGCTGCCCTTCTTGCAAAATTTGTAGTGCCATGCTGCAATCCCATGATGAC 300
 DB 267 TGGATGTTTGGGCTGCCCTTCTTGCAAAATTTGTAGTGCCATGCTGCAATCCCATGATGAC 326
 QY 301 CTCACGTTCCCTATTCTATGTGGTGCATCTGCTGCAACCATGCTGCTTCTTCAAGTGC 360
 DB 327 CTCACGTTCCCTATTCTATGTGGTGCATCTGCTGCAACCATGCTGCTTCTTCAAGTGC 386
 QY 361 AAAGACAAAGTGGAAATCTCAGAGAAACTGCTGCTGGCTGCAAGTGGCTGGCATGTTGG 420
 DB 387 AAAGACAAAGTGGAAATCTCAGAGAAACTGCTGCTGGCTGCAAGTGGCTGGCATGTTGG 446
 QY 421 AGCTGGTGGTATGTCATTTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 480
 DB 447 AGCTGGTGGTATGTCATTTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 506
 QY 481 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 540
 DB 507 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 566
 QY 541 ATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 567 ATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626
 QY 601 GTCCTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 660
 DB 627 GTCCTTCATCATTTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 686
 QY 661 TTCTGGGCTCAGCTGAAAAAACCCTATTTTATAGGGTGCATCTTGTGTTTGTCTTCTTCTTCTTCT 720
 DB 687 TTCTGGGCTCAGCTGAAAAAACCCTATTTTATAGGGTGCATCTTGTGTTTGTCTTCTTCTTCTTCT 746
 QY 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGACGCAATTCATGCTGTTAAACAGC 780
 DB 747 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGACGCAATTCATGCTGTTAAACAGC 806
 QY 781 AAGTTGCAATTTATACGAAATCTTTTGTAGTGTAAACAGCAATAGCTGCTATGATTTG 840
 DB 807 AAGTTGCAATTTATACGAAATCTTTTGTAGTGTAAACAGCAATAGCTGCTATGATTTG 866
 QY 841 CTTCTCTTTGCTTTGGGGGAGCCATGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
 DB 867 CTTCTCTTTGCTTTGGGGGAGCCATGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 926
 QY 901 TGTGTTTGTGCGGTTAG 918
 DB 927 TGTGTTTGTGCGGTTAG 944
 RESULT 11
 ADC86554
 ID ADC86554 standard; DNA; 113306 BP.
 XX
 AC ADC86554;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human GPCR gene SEQ ID NO:1007.
 XX ds; gene; human; GPCR;
 KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
 XX Homo sapiens.
 XX EP1270724-A2.
 PN

neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 attention deficit-hyperactivity disorder/attention deficit disorder;
 parkinson's disease; migraine; senile dementia; inflammatory disease;
 rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 neuroprotective; ds.
 Homo sapiens.
 WO200136473-A2.
 25-MAY-2001.
 16-NOV-2000; 2000WO-US031591.
 16-NOV-1999; 99US-0165838P.
 17-NOV-1999; 99US-0166071P.
 19-NOV-1999; 99US-0166678P.
 28-DEC-1999; 99US-0173396P.
 22-FEB-2000; 2000US-0184129P.
 28-FEB-2000; 2000US-0185421P.
 28-FEB-2000; 2000US-0185554P.
 02-MAR-2000; 2000US-0186530P.
 03-MAR-2000; 2000US-0186811P.
 09-MAR-2000; 2000US-0188114P.
 17-MAR-2000; 2000US-0190310P.
 21-MAR-2000; 2000US-0190800P.
 20-APR-2000; 2000US-0198568P.
 02-MAY-2000; 2000US-0201139P.
 08-MAY-2000; 2000US-0203111P.
 25-MAY-2000; 2000US-0207094P.
 (PHAA) PHARMACIA & UPJOHN CO.
 Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
 Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Ruff RM;
 WPI; 2001-389826/41.
 P-PSDB; AAG80969.
 New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
 useful for diagnosing and treating e.g. schizophrenia.
 Claim 4; Page 89-90; 261pp; English.
 The present invention relates to novel G protein-coupled receptors
 (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
 31-38, 40, 41, 53-60), and their coding sequences. The present sequence is
 the coding sequence for one such G protein-coupled receptor. GPCRs are
 also known as seven transmembrane receptors and function in signal
 transduction. The nGPCRx coding sequences are useful for screening a
 human to diagnose a disorder affecting the brain or a genetic
 predisposition, specifically schizophrenia. nGPCRx are useful for
 identifying compounds useful for treating schizophrenia. Detection of
 nGPCRx in a sample is useful as a diagnostic tool for diseases or
 disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,
 CNS disorders, infections such as HIV-1, metabolic and cardiovascular,
 diseases, proliferative disorders and hormonal disorders. Modulators of
 nGPCRx activity have the utility for treating neurological disorders,
 including schizophrenia, ADHD/ADD (attention deficit-hyperactivity
 disorder/attention deficit disorder), and neuronal disorders such as
 Alzheimer's disease, Parkinson's disease, migraine and senile dementia.
 Additional disorders include inflammatory conditions (e.g. Crohn's
 disease), rheumatoid arthritis, autoimmune disorders, cancers,
 respiratory ailments such as asthma, and inflammatory diseases e.g.
 inflammatory bowel disease
 Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;
 Query Match 100.0%; Score 918; DB 4; Length 2525;
 Best Local Similarity 100.0%; Pred. No. 6e-261;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ATGCCTGGCCACATACATCCTCCAGGAATTCCTCTTCGGATCCTCATAGTACACCCACTTA 60

XX	19-NOV-2002	(first entry)	
DT	Human GREC-6	cDNA INCYTE ID 90012670CD1	SEQ ID 54.
XX	XX	GREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;	
XX	XX	cytotoxic; neuroprotective; antiparkinsonian; hepatotropic; laxative;	
XX	XX	cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;	
KW	KW	protezoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;	
KW	KW	Parkinson's disease; Crohn's disease; constipation; infection;	
KW	KW	gene therapy; gene; ss.	
XX	OS	Homo sapiens.	
XX	XX	WO200263004-A2.	
PN	XX	15-AUG-2002.	
XX	XX	06-FEB-2002; 2002WO-US003635.	
PF	XX	07-FEB-2001; 2001US-0267322P.	
XX	XX	23-FEB-2001; 2001US-0271215P.	
PR	XX	08-MAR-2001; 2001US-0274551P.	
PR	XX	23-MAR-2001; 2001US-0278507P.	
PR	XX	30-MAR-2001; 2001US-0280597P.	
PR	XX	02-APR-2001; 2001US-0281107P.	
PR	XX	06-APR-2001; 2001US-0282121P.	
XX	XX	(INCY-) INCYTE GENOMICS INC.	
XX	PA	Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;	
XX	PI	Kallick DR, Gandhi AR, Walia NK, Arvizu C, Elliott VS, Hafalia AJA;	
PI	PI	Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;	
PI	PI	Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;	
PI	PI	Warren BA, Yang J, Lee EA, Harland L;	
XX	XX	WPI; 2002-627557/67.	
DR	XX	P-PSDB; AAB71327.	
XX	XX	New human G-protein coupled receptors (GREC), useful for diagnosing or	
PT	PT	treating a disease or condition associated with decreased expression or	
PT	PT	over expression of functional GRECs e.g. cancer, Alzheimer's and	
PT	PT	Parkinson's.	
XX	XX	Claim 115; Page 213-214; 239pp; English.	
XX	XX	This invention describes novel polypeptides which have anti-HIV,	
CC	CC	antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,	
CC	CC	hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,	
CC	CC	antibacterial, fungicide and protezoacide activity. The products of the	
CC	CC	invention are useful for treating a disease or condition associated with	
CC	CC	decreased expression or over expression of functional G-protein coupled	
CC	CC	receptors (GREC), while antibodies generated against the polypeptide of	
CC	CC	the invention are useful for diagnosing a condition or disease associated	
CC	CC	with the expression of GREC e.g. arteriosclerosis, cirrhosis, cancer,	
CC	CC	stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,	
CC	CC	constipation, AIDS, or bacterial, viral, fungal or protozoal infections.	
CC	CC	The compounds described in the invention can be used for gene therapy.	
CC	CC	AAF8580-AAF8627 encode the GREC proteins represented by AAB71322-	
CC	CC	AAB71369, described in the disclosure of the invention	
XX	XX	Sequence 1460 BP; 363 A; 327 C; 316 G; 454 T; 0 U; 0 Other;	
XX	XX	Query Match	
XX	XX	Best Local Similarity 100.0%; Score 918; DB 6; Length 1460;	
XX	XX	Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	QY	1 ATCCCTGGCCACATACCTCCAGGAATTCCTTGGGATCCTATAGTGACACCCCACTTA 60	
DB	DB	343 ATCCCTGGCCACATACCTCCAGGAATTCCTTGGGATCCTATAGTGACACCCCACTTA 402	
QY	QY	61 ATCAGCCTCTACTTATAGTGTATTGGGGCTGGTGGGTCTCATTTCCATTCTTTTC 120	

Db	403	ATCAGCCTCTACTTTCATAGTGTCTATTGGCGGGCTGGTGGGTGTCATTTCCATTCTTTTC	462
QY	121	CTTCCTGGTGAATAATGAACACCCGGTCAGTGACACCATGCGGTCAATTAACCTTGGTGGTG	180
Db	463	CTTCCTGGTGAATAATGAACACCCGGTCAGTGACACCATGCGGTCAATTAACCTTGGTGGTG	522
QY	181	GTCACAGCGTTTCTTCTGTGACAGTGCCATTTTCGCTGACCTACCTCATCAAGAAAGACT	240
Db	523	GTCACAGCGTTTCTTCTGTGACAGTGCCATTTTCGCTGACCTACCTCATCAAGAAAGACT	582
QY	241	TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGTGCACATCCACATGTAC	300
Db	583	TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGTGCACATCCACATGTAC	642
QY	301	CTCACGTTTCTTATGTGTGTGATCTCGGTGTCACAGATACCTCATCTTCTTCAAGTGC	360
Db	643	CTCACGTTTCTTATGTGTGTGATCTCGGTGTCACAGATACCTCATCTTCTTCAAGTGC	702
QY	361	AAAGACAAAGTGAATTTCTACAGAAATCTGATGCTGTGGCTGCGCATGTGGCATGTGG	420
Db	703	AAAGACAAAGTGAATTTCTACAGAAATCTGATGCTGTGGCTGCGCATGTGGCATGTGG	762
QY	421	ACGCTGGTGAATGTCTATGTGTGATCTCGGTGTCACAGATACCTCATCTTCTTCAAGTGC	480
Db	763	ACGCTGGTGAATGTCTATGTGTGATCTCGGTGTCACAGATACCTCATCTTCTTCAAGTGC	822
QY	481	TACAAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC	540
Db	823	TACAAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAATC	882
QY	541	ATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	600
Db	883	ATCAACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	942
QY	601	GCTCTTCATCATATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG	660
Db	943	GCTCTTCATCATATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG	1002
QY	661	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCAATCCTTGTGTGTGTGTGTGTGT	720
Db	1003	TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCAATCCTTGTGTGTGTGTGTGTGT	1062
QY	721	TACCACTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCGAATGCTGTAAACGC	780
Db	1063	TACCACTTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCGAATGCTGTAAACGC	1122
QY	781	AAGTTTGCATTTTATACGAATCTTCTTGAGTGTAAACAGCAATTAGCTGTGATGATTG	840
Db	1123	AAGTTTGCATTTTATACGAATCTTCTTGAGTGTAAACAGCAATTAGCTGTGATGATTG	1182
QY	841	CTTCTCTTTTGTCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT	900
Db	1183	CTTCTCTTTTGTCTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT	1242
QY	901	TGTGTTTGTGCGGTAG 918	
Db	1243	TGTGTTTGTGCGGTAG 1260	
RESULT 9			
AAH51009			
ID	AAH51009	standard; DNA; 2525 BP.	
XX	XX	AAH51009;	
XX	XX	28-AUG-2001 (first entry)	
DT	XX	Human nPCR16 coding sequence #2.	
DE	XX	G protein-coupled receptor; nPCR; seven transmembrane receptor;	
KW	KW	signal transduction; schizophrenia; thyroid disorder; renal failure;	
KW	KW	rheumatoid arthritis; CNS disorder; infection; metabolic disease;	
KW	KW	cardiovascular disease; proliferative disorder; hormonal disorder;	

Db 1119 TGTGTTTGTGCCGTAG 1136

RESULT 7

AAF89584
ID AAF89584 standard; cDNA; 1340 BP.

XX AAF89584;

XX 19-NOV-2002 (first entry)

XX Human GREC-5 cDNA INCYTE ID 90012586CD1 SEQ ID 53.

XX GREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
KW cytosolic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
KW cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;
KW protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
KW Parkinson's disease; Crohn's disease; constipation; infection;
KW gene therapy; gene; ss.

XX Homo sapiens.

OS WO200263004-A2.

XX 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003635.

XX 07-FEB-2001; 2001US-0267322P.

XX 23-FEB-2001; 2001US-0271215P.

XX 08-MAR-2001; 2001US-0274551P.

XX 23-MAR-2001; 2001US-0278507P.

XX 30-MAR-2001; 2001US-0280597P.

XX 02-APR-2001; 2001US-0281107P.

XX 06-APR-2001; 2001US-0282121P.

XX (INCY-) INCYTE GENOMICS INC..

XX Baughn MR, Triboley CM, Nguyen DB, Thornton M, Yao MG;

XX Kallack DA, Gandhi AR, Walia NK, Arvisu C, Elliott VS, Hafalia AJA;

XX Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DM;

XX Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;

XX Warren BA, Yang J, Lee EA, Harland L;

XX WPI; 2002-627557/67.

XX P-PSDB; AAB71326.

XX New human G-protein coupled receptors (GCREC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT over expression of functional GCRECs e.g. cancer, Alzheimer's and
PT Parkinson's.
XX Claim 114; Page 213; 239pp; English.

XX This invention describes novel polypeptides which have anti-HIV.

XX antarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,

XX hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,

XX antibacterial, fungicide and protozoacide activity. The products of the

XX invention are useful for treating a disease or condition associated with

XX decreased expression or over expression of functional G-protein coupled

XX receptors (GCREC), while antibodies generated against the polypeptide of

XX the invention are useful for diagnosing a condition or disease associated

XX with the expression of GREC e.g. arteriosclerosis, cirrhosis, cancer,

XX stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,

XX constipation, AIDS, or bacterial, viral, fungal or protozoal infections.

XX The compounds described in the invention can be used for gene therapy.

XX AAF89580-AAF89627 encode the GCREC proteins represented by AAB71322-

XX AAB71369, described in the disclosure of the invention

XX Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;

Best Local Similarity 100.0%; Pred. No. 4.3e-261;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCCTGGCCACAATACTCCAGGAATTCCTCTTGGATCCTTATAGTGCACACCCACTTA 60
Db 223 ATGCCTGGCCACAATACTCCAGGAATTCCTCTTGGATCCTTATAGTGCACACCCACTTA 282

Qy 61 ATCAGCCTCTACTTCATAGTCTTATTTGGGGCTGGTGGTGTCTATTTCCATCTTTTC 120
Db 283 ATCAGCCTCTACTTCATAGTCTTATTTGGGGCTGGTGGTGTCTATTTCCATCTTTTC 342

Qy 121 CTCCTGGTGAATAAGAACACCCCGTCAGTGAACACCATGGCGGTCAATTAACCTGGTGGTG 180
Db 343 CTCCTGGTGAATAAGAACACCCCGTCAGTGAACACCATGGCGGTCAATTAACCTGGTGGTG 402

Qy 181 GTCACAGCGCTTTCTGTGACAGTGCCTATTTGGTGTGACCTCATCTCATCAGAGAGACT 240
Db 403 GTCACAGCGCTTTCTGTGACAGTGCCTATTTGGTGTGACCTCATCTCATCAGAGAGACT 462

Qy 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
Db 463 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 522

Qy 301 CTCACGTTCCCTATTTATGTTGGTGTCTGTCACAGATACCTCATCTTCTTCAAGTGC 360
Db 523 CTCACGTTCCCTATTTATGTTGGTGTCTGTCACAGATACCTCATCTTCTTCAAGTGC 582

Qy 361 AAAGACAAAGTGGAAATTTCTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG 420
Db 583 AAAGACAAAGTGGAAATTTCTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG 642

Qy 421 ACGCTGGTGTATGTCATTTGTTGGTACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAA 480
Db 643 ACGCTGGTGTATGTCATTTGTTGGTACCCCTGGTGTCTCCGGTATGGAATCCATGAGGAA 702

Qy 481 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTACACATATGGAATC 540
Db 703 TACAATGAGGAGCACTGTTTAAATTTCAAAAGAGCTTGTACACATATGGAATC 762

Qy 541 ATCAACTATATGATAGTCAATTTTGTGCATAGCCGTTGCTGTGATTCCTGTTGGTCTTCCAG 600
Db 763 ATCAACTATATGATAGTCAATTTTGTGCATAGCCGTTGCTGTGATTCCTGTTGGTCTTCCAG 822

Qy 601 GTCTTCATCATATGTTGATGTTGCGAGAGCTAGCCACTCTTTACTATCCACCCAGGAG 660
Db 823 GTCTTCATCATATGTTGATGTTGCGAGAGCTAGCCACTCTTTACTATCCACCCAGGAG 882

Qy 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCCTGTTGTTTCTTCCC 720
Db 883 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCCTGTTGTTTCTTCCC 942

Qy 721 TACAGTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTACAGC 780
Db 943 TACAGTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTACAGC 1002

Qy 781 AAGTTCCATTTTATACGAAATCTTCTTCAGTGTAAACAGCAATTAGCTCTATGATTG 840
Db 1003 AAGTTCCATTTTATACGAAATCTTCTTCAGTGTAAACAGCAATTAGCTCTATGATTG 1062

Qy 841 CTTCCTCTTTCTTTGGGGAAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Db 1063 CTTCCTCTTTCTTTGGGGAAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 1122

Qy 901 TGTGTTTGTGCGGTAG 918
Db 1123 TGTGTTTGTGCGGTAG 1140

RESULT 8
AAF89585
ID AAF89585 standard; cDNA; 1460 BP.

XX AAF89585;

AC AAF89585;

Query Match

100.0%; Score 918; DB 6; Length 1340;

QY 661 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGTTCATCTTTGTTTCTTCTCC 720
 Db 661 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGTTCATCTTTGTTTCTTCTCC 720
 QY 721 TACCAAGTCTTTAGGATCTATTACTTGAATGTTGAGCGCATCCCAATGCTGTAACAGC 780
 Db 721 TACCAAGTCTTTAGGATCTATTACTTGAATGTTGAGCGCATCCCAATGCTGTAACAGC 780
 QY 781 AAGGTTGCAATTTTAAACCAAACTCTTTGAGTGTAAACAGCAATAGCTGCTATGATTG 840
 Db 781 AAGGTTGCAATTTTAAACCAAACTCTTTGAGTGTAAACAGCAATAGCTGCTATGATTG 840
 QY 841 CTTCTCTTTGCTTTGCGGGAAGCCATTTGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 900
 Db 841 CTTCTCTTTGCTTTGCGGGAAGCCATTTGTTTAAAGCAAAAGATAATTGGCTTATGGAAT 900
 QY 901 TGTGTTTTCGCGTTAG 918
 Db 901 TGTGTTTTCGCGTTAG 918

RESULT 5
 AAL57070
 ID AAL57070 standard; DNA; 1040 BP.
 XX AAL57070;
 XX
 DT 17-SEP-2003 (first entry)
 XX Human G-protein coupled receptor GAVE18 DNA sequence.
 DE
 KW Human G-protein coupled receptor; GAVE18; signal transduction;
 KW inflammation; physiological immunological response; antiinflammatory;
 KW antiasthmatic; antirheumatic; antiarthritic; antisense therapy;
 KW chromosomal mapping; tissue typing; forensic biology;
 KW predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;
 KW rheumatoid arthritis; gene; ds.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..918
 FT CDS /*tag= a
 FT /product= "GAVE18 protein"
 XX
 PN WO2003042399-A2.
 XX
 PD 22-MAY-2003.
 XX
 PF 08-NOV-2002; 2002WO-US035887.
 XX
 PR 13-NOV-2001; 2001US-0354150P.
 PR 22-MAR-2002; 2002GB-00006891.
 XX
 XX (AVET) AVENTIS PHARM INC.
 PA
 PI Eishengdrelo H, Cai J, Busch SJ, Gassenhuber J;
 XX
 XX WPI: 2003-457496/43.
 DR P-PSDB; AA027265.
 XX
 XX New GAVE18 polypeptide and nucleic acid molecule encoding the
 PT polypeptide, useful for preventing and treating a disease or disorder
 PT associated with aberrant expression or activity of GAVE18, e.g. asthma or
 PT rheumatoid arthritis.
 XX
 XX Claim 1; Fig 5; 88pp; English.
 PS
 CC This invention relates to a novel G-protein coupled receptor (GAVE18)
 CC that is involved in signal transduction in respect to inflammation and
 CC the physiological immunological response. Molecules which may modulate
 CC the signalling activity or signal transduction of the receptor may be

antiinflammatory, antiasthmatic, antirheumatic or antiarthritic. The
 CC GAVE18 receptor and the DNA sequence encoding it may be a target for
 CC antisense therapy or gene therapy. The nucleic acid molecule, GAVE18
 CC proteins and antibodies may be useful in screening assays, detection
 CC assays (for example chromosomal mapping, tissue typing or forensic
 CC biology), or predictive medicine (for example diagnostic assays,
 CC prognostic assays, monitoring clinical trials and pharmacogenomics. The
 CC nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse
 CC agonist and antagonist are also useful for preventing and treating a
 CC disease or disorder associated with aberrant expression or activity of
 CC GAVE18, such as inflammation and immunological-related diseases or
 CC disorders, for example asthma, chronic obstructive pulmonary disease or
 CC rheumatoid arthritis. The present sequence is the DNA sequence encoding
 CC the GAVE18 protein of the invention
 XX
 SQ Sequence 1040 BP; 289 A; 216 C; 213 G; 322 T; 0 U; 0 Other;
 Query Match 100.0%; Score 918; DB 8; Length 1040;
 Best Local Similarity 100.0%; Pred. No. 3.7e-261;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCTGGCCACAAATACCTCAGGAATTCCTCTTGGATCCTATAGTGACACCCACTTA 60
 Db 1 ATGCTGGCCACAAATACCTCAGGAATTCCTCTTGGATCCTATAGTGACACCCACTTA 60
 QY 61 ATCAGCCTCTACTTCATAGTGTCTTATTGGCGGCTGTGGTGGTGCATTTCCATTCTTTTC 120
 Db 61 ATCAGCCTCTACTTCATAGTGTCTTATTGGCGGCTGTGGTGGTGCATTTCCATTCTTTTC 120
 QY 121 CTCCTGTGAAATGAACACCCGGTCAGTGACCAACATGGCGGTCATTAATCTGGTGGTG 180
 Db 121 CTCCTGTGAAATGAACACCCGGTCAGTGACCAACATGGCGGTCATTAATCTGGTGGTG 180
 QY 181 GTCCACAGCGTTTTTCGTGACAGTGCCTTTCGTTGACCTACCTCATCAAGAAGACT 240
 Db 181 GTCCACAGCGTTTTTCGTGACAGTGCCTTTCGTTGACCTACCTCATCAAGAAGACT 240
 QY 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTSCCAATGCTGCACATCCACATGTAC 300
 Db 241 TGGATGTTGGGCTGCCCTTCTGCAAAATTTGTGAGTSCCAATGCTGCACATCCACATGTAC 300
 QY 301 CTCAGTTCCTATTCTATGTGTGCTGTCCTGTCACAGATACCTCATCTTCTTCAAGTGC 360
 Db 301 CTCAGTTCCTATTCTATGTGTGCTGTCCTGTCACAGATACCTCATCTTCTTCAAGTGC 360
 QY 361 AAACACAAAGTGGAAATCTACAGAAATCTCATGCTGTGGTGCAGTGTGGCATGTGG 420
 Db 361 AAACACAAAGTGGAAATCTACAGAAATCTCATGCTGTGGTGCAGTGTGGCATGTGG 420
 QY 421 ACGCTGTGATGTTCATGTGTGATACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480
 Db 421 ACGCTGTGATGTTCATGTGTGATACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480
 QY 481 TACAATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 540
 Db 481 TACAATGAGGAGCACTGTTTTAAATTTCAAAAGAGCTTGTCTTACACATATGTGAAATC 540
 QY 541 ATCAACTATATGATGATGATCTTTTGTGATAGCGGTGTCTGTGATCTGTGGTCTTCCAG 600
 Db 541 ATCAACTATATGATGATGATCTTTTGTGATAGCGGTGTCTGTGATCTGTGGTCTTCCAG 600
 QY 601 GTCTTCATCATTTATGTTGATGCTGCAAGCTACCGCCTCTTTTACTATCCACCCAGGAG 660
 Db 601 GTCTTCATCATTTATGTTGATGCTGCAAGCTACCGCCTCTTTTACTATCCACCCAGGAG 660
 QY 661 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGTTCATCTTTGTTTCTTCTCC 720
 Db 661 TTCTGGGCTCAGCTGAAACCACTATTTTATAGGGTTCATCTTTGTTTCTTCTCC 720
 QY 721 TACCAAGTCTTTAGGATCTATTACTTGAATGTTGAGCGCATCCCAATGCTGTAACAGC 780
 Db 721 TACCAAGTCTTTAGGATCTATTACTTGAATGTTGAGCGCATCCCAATGCTGTAACAGC 780

```
Db 361 AAAGACAAAGTGAATTTACAGAAATGTCATGCTGTGGCTGCCAGTGTGGCATGTGG 420
Qy 421 AGCTGGTGTATGTCATTTGTTGTTACCCCTGGTGTCTCCCGTATGGAATCCATGAGAA 480
Db 421 AGCTGGTGTATGTCATTTGTTGTTACCCCTGGTGTCTCCCGTATGGAATCCATGAGAA 480
Qy 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTTCACATATGTGAAATC 540
Db 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTTCACATATGTGAAATC 540
Qy 541 ATCAACTATATGATGTCATTTTGTTCATAGCCGTTGCTGTGATCTGTGTCCTCCAG 600
Db 541 ATCAACTATATGATGTCATTTTGTTCATAGCCGTTGCTGTGATCTGTGTCCTCCAG 600
Qy 601 GTCTTCATCATTTATGTTGTCAGAGAGTACGCCACTCTTTACTATCCACAGGAG 660
Db 601 GTCTTCATCATTTATGTTGTCAGAGAGTACGCCACTCTTTACTATCCACAGGAG 660
Qy 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTCATCTTTGTTGTTCTTCCC 720
Db 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTCATCTTTGTTGTTCTTCCC 720
Qy 721 TACCAGTCTTTAGGATCTATTACTTGAATGTTGTAGCGCATTCCAATGCCCTGTAAACAGC 780
Db 721 TACCAGTCTTTAGGATCTATTACTTGAATGTTGTAGCGCATTCCAATGCCCTGTAAACAGC 780
Qy 781 AAGTTGCAATTTATTAACGAATCTTTGAGTGTAAAGCAATGAGCTGTATGATTTG 840
Db 781 AAGTTGCAATTTATTAACGAATCTTTGAGTGTAAAGCAATGAGCTGTATGATTTG 840
Qy 841 CTCTCTTTGTTCTTTGGGGGAGCCATTTGTTTAAAGCAATGAGCTGTATGATTTG 900
Db 841 CTCTCTTTGTTCTTTGGGGGAGCCATTTGTTTAAAGCAATGAGCTGTATGATTTG 900
Qy 901 TGTGTTTGTGCGGTAG 918
Db 901 TGTGTTTGTGCGGTAG 918
```

RESULT 4

```
ID ABZ59171 standard; DNA; 918 BP.
XX
AC ABZ59171;
XX
DT 28-APR-2003 (first entry)
XX
DE Human TGR343 protein encoding DNA.
XX
KW G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;
KW TGR358; antidiabetic; neuroprotective; cerebroprotective; nephroprotective;
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;
KW immunosuppressive; antiinflammatory; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..918
FT /tag= a
FT /product= "TGR343"
XX
PN WO2003004678-A2.
XX
XX
PD 16-JAN-2003.
XX
PF 01-JUL-2002; 2002WO-US020860.
XX
PR 03-JUL-2001; 2001US-0302800P.
XX
PA (TULA-) TULARIK INC.
XX
PI Tian H, Dai K, Chen J, Zhao J, Cutler G;
XX
```

```
DR WPI; 2003-210369/20.
DR P-PSDB; ABP71378.
XX
PT New G-protein coupled receptor polypeptides designated TGR2, TGR38,
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or
PT nephrolithiasis.
XX
PS Claim 7; Page 61; 74pp; English.
XX
CC The invention provides new G-protein coupled receptor (GPCR) polypeptides
CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding
CC polynucleotides. The polypeptides can be expressed by standard DNA
CC recombination methodology. The polypeptides are useful for screening or
CC identifying modulators of GPCR or signal transduction. The modulators of
CC signal transduction are useful for treating or preventing TGR-associated
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The
CC polypeptides are useful as targets for diagnosing or treating e.g.
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia,
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,
CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute
CC inflammatory dermatoses. The present sequence represents a human TGR343
CC protein encoding DNA
XX
SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
Query Match 100.0%; Score 918; DB 7; Length 918;
Best Local Similarity 100.0%; Pred. No. 3.5e-261;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGGATCTATAGTACACCCCACTTA 60
Db 1 ATGCTGGCCACAAATACCTCCAGGAATTCCTCTTGGGATCTATAGTACACCCCACTTA 60
Qy 61 ATCAGCCTCTACTATAGTGTCTTATTTGGCGGCTGTGGGTGTCTATTTCCATCTTTTC 120
Db 61 ATCAGCCTCTACTATAGTGTCTTATTTGGCGGCTGTGGGTGTCTATTTCCATCTTTTC 120
Qy 121 CTCCTGTGAAATGAACACCCGTCAGTGACACCATGCGGTCTTAACTTGGTGGTG 180
Db 121 CTCCTGTGAAATGAACACCCGTCAGTGACACCATGCGGTCTTAACTTGGTGGTG 180
Qy 181 GTCACAGCCTTTTCTGTGACAGTGCCATTTGCTTGGCTTACCTCATCAAGAAGACT 240
Db 181 GTCACAGCCTTTTCTGTGACAGTGCCATTTGCTTGGCTTACCTCATCAAGAAGACT 240
Qy 241 TGGATGTTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGTGCACATCCACATGTAC 300
Db 241 TGGATGTTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGTGCACATCCACATGTAC 300
Qy 301 CTCACGTTCTTATTTATGTTGTCCTCTGTCAGTCCATTTGCTTACCTCATCAAGAAGACT 360
Db 301 CTCACGTTCTTATTTATGTTGTCCTCTGTCAGTCCATTTGCTTACCTCATCAAGAAGACT 360
Qy 361 AAAGACAAAGTGAATTTACAGAAATGTCATGCTGTGGCTGCCAGTGTGGCATGTGG 420
Db 361 AAAGACAAAGTGAATTTACAGAAATGTCATGCTGTGGCTGCCAGTGTGGCATGTGG 420
Qy 421 ACCTGCTGATTTGTCATTTGTCATCCCTGTTGTCTCCCGTATGGAATCCATGAGAA 480
Db 421 ACCTGCTGATTTGTCATTTGTCATCCCTGTTGTCTCCCGTATGGAATCCATGAGAA 480
Qy 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTTCACATATGTGAAATC 540
Db 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTTCACATATGTGAAATC 540
Qy 541 ATCAACTATATGATGTCATTTTGTTCATAGCCGTTGCTGTGATCTGTGTCCTCCAG 600
Db 541 ATCAACTATATGATGTCATTTTGTTCATAGCCGTTGCTGTGATCTGTGTCCTCCAG 600
Qy 601 GTCTTCATCATTTATGTTGTCAGAGAGTACGCCACTCTTTTACTATCCACAGGAG 660
Db 601 GTCTTCATCATTTATGTTGTCAGAGAGTACGCCACTCTTTTACTATCCACAGGAG 660
```



```
Db      1 ATGCCTGGCCCAATACACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60
Qy      61 ATCAGCCTCTACTTCATAGTGCTTATTTGGCGGGCTGGTGGTGGTCAATTTCCATCTTTTC 120
Db      61 ATCAGCCTCTACTTCATAGTGCTTATTTGGCGGGCTGGTGGTGGTCAATTTCCATCTTTTC 120
Qy      121 CTCCTGGTGAAATGAACACCCGGTCAAGTACACACCATGGCGGTCAATTAACCTGGTGGTG 180
Db      121 CTCCTGGTGAAATGAACACCCGGTCAAGTACACACCATGGCGGTCAATTAACCTGGTGGTG 180
Qy      181 GTCACAGCGTTTCTTCTGTGACAGTGCCATTTCCCTTGAACCTCATCAAGAAGACT 240
Db      181 GTCACAGCGTTTCTTCTGTGACAGTGCCATTTCCCTTGAACCTCATCAAGAAGACT 240
Qy      241 TGGATGTTTGGCGCTCCCTTCGCAAAATTTGAGTGCATCTGCTGCACATCCACATGATAC 300
Db      241 TGGATGTTTGGCGCTCCCTTCGCAAAATTTGAGTGCATCTGCTGCACATCCACATGATAC 300
Qy      301 CTCAGGTTCTTATCTATGCTGATCTCTGTCACAGATACCTCATCTTCAAGTGC 360
Db      301 CTCAGGTTCTTATCTATGCTGATCTCTGTCACAGATACCTCATCTTCAAGTGC 360
Qy      361 AAAGACAAGTGGAAATCTACAGAAATCTGATGCTGCTCCGGTATGGAATCCATGAGAA 420
Db      361 AAAGACAAGTGGAAATCTACAGAAATCTGATGCTGCTCCGGTATGGAATCCATGAGAA 420
Qy      421 AGCTGGTGATGTCATGTTGTTACCTCCCTGGTGTCTCCGGTATGGAATCCATGAGAA 480
Db      421 AGCTGGTGATGTCATGTTGTTACCTCCCTGGTGTCTCCGGTATGGAATCCATGAGAA 480
Qy      481 TACAATGAGGAGCACTGTTTAAATTCACAAAGCTGCTTACACATATGTGAAATC 540
Db      481 TACAATGAGGAGCACTGTTTAAATTCACAAAGCTGCTTACACATATGTGAAATC 540
Qy      541 ATCAACTATATGATGATCTATTTCTGTCATAGCCGTTGCTGTGATTCGTGCTCTCCAG 600
Db      541 ATCAACTATATGATGATCTATTTCTGTCATAGCCGTTGCTGTGATTCGTGCTCTCCAG 600
Qy      601 GCTTTCATCATTTATGTTGATGTCAGAGCTPACGCCACTCTTTACTATPCCACAGAG 660
Db      601 GCTTTCATCATTTATGTTGATGTCAGAGCTPACGCCACTCTTTACTATPCCACAGAG 660
Qy      661 TTCGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTGTTGTTTCTTCTTCCC 720
Db      661 TTCGGGCTCAGCTGAAACCTATTTTATAGGGTCACTCTGTTGTTTCTTCTTCCC 720
Qy      721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCGAATGCCCTGTAACAGC 780
Db      721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCGAATGCCCTGTAACAGC 780
Qy      781 AAGTTGCATTTTATAACGAATCTCTTGATGTTGATGTTGATGTTGATGTTGATGTTG 840
Db      781 AAGTTGCATTTTATAACGAATCTCTTGATGTTGATGTTGATGTTGATGTTGATGTTG 840
Qy      841 CTCTCTTTGCTTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Db      841 CTCTCTTTGCTTTTGGGGAGCCATTTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
Qy      901 TGTGTTTGGCGGTAG 918
Db      901 TGTGTTTGGCGGTAG 918
```

RESULT 3

ID ABT04867 standard; cDNA; 918 BP.

XX AC

XX ABT04867;

XX DT

11-OCT-2002 (first entry)

DE Human G protein coupled receptor hrUP29 coding sequence.

XX

Human; G-protein coupled receptor; GPCR; hrUP28; hrUP29; hrUP30; hrUP31;
hrUP32; hrUP33; hrUP34; hrUP35; hrUP36; hrUP37; gene; ss.
Homo sapiens.
WO200242461-A2.

30-MAY-2002.
26-NOV-2001; 2001WO-US044386.

27-NOV-2000; 2000US-0253404P.
12-DEC-2000; 2000US-0255366P.
20-FEB-2001; 2001US-0270266P.

20-FEB-2001; 2001US-0270286P.
06-APR-2001; 2001US-0282032P.
06-APR-2001; 2001US-0282356P.

06-APR-2001; 2001US-0282358P.
06-APR-2001; 2001US-0282365P.
14-MAY-2001; 2001US-0290917P.

31-JUL-2001; 2001US-0309208P.

(AREN-) ARENA PHARM INC.

Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;

WPI; 2002-566565/60.

P-PSDB; ABJ04069.

Novel endogenous and non-endogenous versions of G protein-coupled

receptor useful for identification of candidate compounds as receptor

agonists or antagonists for use as therapeutic agents.

Claim 7; Page 56-57; 84pp; English.

The present invention provides the protein and coding sequences of

several human G-protein coupled receptors (GPCRs). These can be used in

the identification of candidate compounds as receptor agonists or inverse

agonists having applicability as therapeutic agents. The present sequence

is a GPCR coding sequence of the invention

Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 6; Length 918;

Best Local Similarity 100.0%; Pred. No. 3.5e-261;

Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCCTGGCCCAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60

1 ATGCCTGGCCCAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCCACTTA 60

61 ATCAGCCTCTACTTCATAGTGCTTATTTGGCGGGCTGGTGGTGGTCAATTTCCATCTTTTC 120

61 ATCAGCCTCTACTTCATAGTGCTTATTTGGCGGGCTGGTGGTGGTCAATTTCCATCTTTTC 120

121 CTCCTGGTGAATGAACACCCGGTCAAGTACACCATGGCGGTCAATTAACCTGGTGGTG 180

121 CTCCTGGTGAATGAACACCCGGTCAAGTACACCATGGCGGTCAATTAACCTGGTGGTG 180

181 GTCACAGCGTTTCTTCTGTGACAGTGCCATTTCCCTTGAACCTCATCAAGAAGACT 240

181 GTCACAGCGTTTCTTCTGTGACAGTGCCATTTCCCTTGAACCTCATCAAGAAGACT 240

241 TGGATGTTTGGCGCTCCCTTCGCAAAATTTGAGTGCATCTGCTGCACATCCACATGATAC 300

241 TGGATGTTTGGCGCTCCCTTCGCAAAATTTGAGTGCATCTGCTGCACATCCACATGATAC 300

301 CTCACGTTCTTCTATGTTGATGCTGTCCTGGTGCACAGATACCTCATCTTCTCAAGTGC 360

301 CTCACGTTCTTCTATGTTGATGCTGTCCTGGTGCACAGATACCTCATCTTCTCAAGTGC 360

361 AAAGACAAGTGGAAATCTACAGAAATCTGATGCTGCTCCGGTATGGAATCCATGAGTGC 420

|||||

CC The present invention provides the protein and coding sequences of a
 CC novel human testis-originated G protein-coupled receptor protein TR10.
 CC The sequences can be used in the development of drugs for the treatment
 CC of diseases of the central nervous system, inflammations, diseases of the
 CC circulatory system, cancer, metabolic diseases, immunological diseases,
 CC and diseases of the gastrointestinal system. The present sequence is the
 CC coding sequence of the invention
 XX
 SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 6; Length 918;
 Best Local Similarity 100.0%; Pred. No. 3.5e-261;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCTGGCCACATACCTCCAGCAATTCCTCTGGCATCTATAGTACACCCCACTTA	60
Db	1	ATGCTGGCCACATACCTCCAGCAATTCCTCTGGCATCTATAGTACACCCCACTTA	60
Qy	61	ATCAGCCTCTACTCATAGTCTTATTTGGGGGCTGTGGTGTCTATTCATTCCTTTTC	120
Db	61	ATCAGCCTCTACTCATAGTCTTATTTGGGGGCTGTGGTGTCTATTCATTCCTTTTC	120
Qy	121	CTCTGTGTGAATGAACACCCGCTCAGTGACCAACATGGGCTCATTAATCTTGGTGGTG	180
Db	121	CTCTGTGTGAATGAACACCCGCTCAGTGACCAACATGGGCTCATTAATCTTGGTGGTG	180
Qy	181	GTCCACAGCGTTTCTCTGCTGACAGTGCCATTTTCGCTTGACCTACCTCATCAAGAGACT	240
Db	181	GTCCACAGCGTTTCTCTGCTGACAGTGCCATTTTCGCTTGACCTCATCAAGAGACT	240
Qy	241	TGGATGTTGGGCTGCCCTCTGCAAAATTTGTAGTGCCATGTGCACATCCACATGTAC	300
Db	241	TGGATGTTGGGCTGCCCTCTGCAAAATTTGTAGTGCCATGTGCACATCCACATGTAC	300
Qy	301	CTCAGCTTCTATTTCTATGTTGGTGATCTCTGTCACCAAGATACCTCATCTTCTCAAGTGC	360
Db	301	CTCAGCTTCTATTTCTATGTTGGTGATCTCTGTCACCAAGATACCTCATCTTCTCAAGTGC	360
Qy	361	AAGACAAAGTGAATTTCTACAGAAATCTGATCTGTGCTGCTGCTGCTGCTGCTGCTG	420
Db	361	AAGACAAAGTGAATTTCTACAGAAATCTGATCTGTGCTGCTGCTGCTGCTGCTGCTG	420
Qy	421	ACGCTGTGATGTTGATGTTGGTACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
Db	421	ACGCTGTGATGTTGATGTTGGTACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
Qy	481	TACAAATGAGGAGCACTGTTTAAATTTTCAAGAGCTTCTGTACACATATGTGAATTC	540
Db	481	TACAAATGAGGAGCACTGTTTAAATTTTCAAGAGCTTCTGTACACATATGTGAATTC	540
Qy	541	ATCAACTATATGATGATCATTTTGTATAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600
Db	541	ATCAACTATATGATGATCATTTTGTATAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600
Qy	601	GTCTTCATCATATGTTGATGTCAGAGTACGCCACTCTTTTACTATCCCAACAGGAG	660
Db	601	GTCTTCATCATATGTTGATGTCAGAGTACGCCACTCTTTTACTATCCCAACAGGAG	660
Qy	661	TTCTGGGCTCAGTGAAACCTATTTTATAGGGGTCTACTCTGTTGTTTCTTCTTCC	720
Db	661	TTCTGGGCTCAGTGAAACCTATTTTATAGGGGTCTACTCTGTTGTTTCTTCTTCC	720
Qy	721	TACCAAGTCTTTAGGATCTATTACTGAATGTTGTAGCGATTCCTGCTGCTGCTGCTG	780
Db	721	TACCAAGTCTTTAGGATCTATTACTGAATGTTGTAGCGATTCCTGCTGCTGCTGCTG	780
Qy	781	AAGTTGCAATTTTATACGAATCTTCTGAGTGTAACAGCAATTAGCTCTATGATTG	840
Db	781	AAGTTGCAATTTTATACGAATCTTCTGAGTGTAACAGCAATTAGCTCTATGATTG	840
Qy	841	CTTCTCTTCTTCTTGGGGAGGCAATTTGGTTTAAAGCAAGATAATTTGGCTTATGGAAT	900
Db	841	CTTCTCTTCTTCTTGGGGAGGCAATTTGGTTTAAAGCAAGATAATTTGGCTTATGGAAT	900

Qy 901 TGTGTTTGTGCGGTAG 918
 Db 901 TGTGTTTGTGCGGTAG 918

RESULT 2

ABAA00160
 ID ABA00160 standard; cDNA; 918 BP.

XX ABA00160;

XX 15-NOV-2002 (first entry)

XX PFI-021 cDNA.

XX DE DE
 XX KW KW
 KW KW
 KW KW
 KW KW
 KW KW
 XX CS
 XX XX

Genes; human; G-protein coupled receptor; GPCR; PFI-021;
 peripheral blood mononuclear cell; PBMC; breast; inflammation; allergy;
 respiratory; neurology; psychology; urogenital disease;
 reproductive dysfunction; sexual dysfunction; cancer; tissue repair;
 dermatology; skin pigmentation; photoaging; frailty; osteoporosis;
 metabolic disease; cardiovascular disease; sleep disorder; hair loss;
 gastrointestinal disease; anti-infection; sensory organ disorder; ss.

Homo sapiens.

Key Key Location/Qualifiers
 CDS 1..918
 FT /*tag= a
 FT /product= "PFI-021"

XX EPI225183-A2.

XX 24-JUL-2002.

XX 09-JAN-2002; 2002EP-00250128.

XX 23-JAN-2001; 2001GB-00001739.

XX (PFIZ) PFIZER LTD.

XX (PFIZ) PFIZER INC.

XX Harland L;

XX WPI; 2002-601226/65.

XX P-PSDB; AAG79446.

XX New human G-protein coupled receptor involved in signal transduction,
 PT useful to treat disorders associated with its expression or activity such
 PT as inflammation, allergy and cancer.

XX Claim 1; Fig 1; 8pp; English.

XX This sequence encodes a human G-protein coupled receptor (GPCR), PFI-021.
 CC Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA
 CC libraries from peripheral blood mononuclear cells. Two ESTs have been
 CC identified in libraries derived from breast mRNA. PFI-021 and the
 CC corresponding cDNA are used to treat a patient needing altered activation
 CC or expression of a GPCR, such as inflammation, allergy and respiratory,
 CC neurology, psychology, urogenital disease, reproductive and sexual
 CC dysfunction/disorders, cancer, tissue repair, dermatology, skin
 CC pigmentation disorders, photoaging, frailty, osteoporosis, metabolic
 CC disease, cardiovascular disease, gastro-intestinal disease, anti-
 CC infection, sensory organ disorders, sleep disorders and hair loss
 XX
 SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 6; Length 918;
 Best Local Similarity 100.0%; Pred. No. 3.5e-261;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGGCCACATACCTCCAGCAATTCCTCTGGCATCTATAGTACACCCCACTTA 60
 |||||
 |||||

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 09:09:59 ; Search time 451 Seconds

(without alignments)

8647.108 Million cell updates/sec

Title: US-10-055-106c-1

Perfect score: 918

Sequence: 1 atgctgcccacataacctc.....attgtgttttgcgcgttag 918

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 337863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	6	AAL44713 Human tes
2	918	100.0	918	6	ABA00160 Human tes
3	918	100.0	918	6	ABT04867 Human G p
4	918	100.0	918	7	ABZ59171 Human TGR
5	918	100.0	1040	8	AAL57070 Human G-p
6	918	100.0	1336	6	Aaf88583 Human GCR
7	918	100.0	1340	6	Aaf88584 Human GCR
8	918	100.0	1460	6	Aaf88585 Human GCR
9	918	100.0	2525	4	AAL51009 Human GCR
10	918	100.0	2525	6	ABT570242 DNA encod
11	918	100.0	113306	9	ADC86554 Human GPC
12	916.4	99.8	1051	6	ABK87351 Human GPC
13	916.4	99.8	1684	6	AAL53413 1684 nt c
14	913.4	99.5	939	6	AAL53414 939 nt co
15	895	97.5	1499	6	AAD37670 Human G-p
16	890	75.2	372	9	ADC12789 Human GPC
17	560.8	61.1	810	9	ADB78584 Mouse G-p
18	390	42.5	447	4	AAL50979 Human GCR
19	390	42.5	447	6	ABT70212 DNA encod
20	162	17.6	479	4	AAL56763 Human lrm
21	144.8	15.8	897	7	ABZ23663 G protein
22	76.4	8.3	1113	5	ABI98010 Non-endog
23	76.4	8.3	1805	6	ABS53446 CDNA enco

ALIGNMENTS

RESULT 1

AAL44713
ID AAL44713 standard; DNA; 918 BP.

AC AAL44713;

DT 03-MAY-2002 (first entry)

DE Human testis originated G-protein coupled receptor TGR10 coding sequence.

KW Human; testis-originated G-protein coupled receptor; TGR10; inflammatory;
cystostatic; immunomodulator; cardiac; neuroprotective; Gene therapy;
inflammation; nervous system disease; circulatory system disease; cancer;
metabolic disease; immunological disease; gastrointestinal disease; gene;
ds.

OS Homo sapiens.

EH Key Location/Qualifiers
CDS I. 918

FT /*tag= a

FT /product= "TGR10"

XX WO200196567-A1.

XX PD 20-DEC-2001.

XX PF 14-JUN-2001; 2001WO-JP005061.

XX PR 15-JUN-2000; 2000JP-00184596.

XX PR 19-JUL-2000; 2000JP-00223887.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Moriya T, Ito T, Shintani Y, Miyajima N;

XX DR WPI; 2002-098071/13.

XX DR P-PSDB; AAM48989.

XX Human testis-originated G protein-coupled receptor protein TGR10 and
PT encoded DNA, useful for gene diagnosis and developing drugs to treat e.g.
PT diseases of central nervous system, inflammations and diseases of
PT circulatory system.

XX PS Claim 5; Page 99; 110pp; Japanese.

XX

24 76.4 8.3 1829 7 ABX94264 Human orp
25 76.4 8.3 1829 7 ABX94262 Human orp
26 76.4 8.3 1829 7 ABX94263 Human orp
27 76.4 8.3 1973 7 ACA56793 Human sig
28 76.4 8.3 2534 9 ADC40517 DNA deriv
29 76.4 8.3 2534 7 ABX94045
30 76.4 8.3 2534 7 ABZ42709 Human op1
31 74.8 8.1 1829 7 ABX94260 Human orp
32 73.2 7.6 1177 3 AAZ60659 DNA encod
33 70.2 7.6 1177 3 AAZ60658 DNA encod
34 69.6 7.6 2602 7 ABX94254 Human orp
35 68 7.4 1947 7 ABX94261 Human orp
36 61 6.6 1143 5 ABI98011 Non-endog
37 61 6.6 1182 7 ACA56819 Human sig
38 61 6.6 1182 7 ABZ42678 Human op1
39 61 6.6 1182 9 AAD58490 Human kap
40 61 6.6 1182 9 ADE84861 Farnesyl
41 59.8 6.5 1243 7 ABX94042 Rat orpha
42 59.8 6.5 1330 2 AAQ75928 Mouse op1
43 59.8 6.5 1387 7 ABX94039 Rat orpha
44 59.8 6.5 1567 2 AAQ89233 Rat op1o1
45 59.8 6.5 1567 3 AAA59510 CDNA enco

XX 28-FEB-2002; 2002MO-US006455.
XX 01-MAR-2001; 2001US-0272677P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Glucksmann MA;
XX WPI; 2002-732793/79.
XX P-PSDB; AAO22919.
XX New G-protein coupled receptor used in receptor assays as a target for
PT diagnosis and treatment of receptor-mediated disorders, e.g. immune and
PT inflammatory disorders, platelet disorders, skeletal or bone metabolism
PT disorders.
XX Claim 5; Page 101-103; 105pp; English.
XX The invention relates to an isolated polypeptide, which is a G-protein
CC coupled receptor (GPCR) related to subfamily I of G-protein coupled
CC receptor type proteins (GPCRs), designated the 93870 receptor. The
CC polypeptides, nucleic acid molecules and antibodies of the invention are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC monitoring clinical trials or pharmacogenetics), or in methods of
CC treatment (e.g. therapeutic and prophylactic). They are useful in
CC treating and diagnosing conditions related to aberrant activity or
CC expression of the 93870 polypeptides or nucleic acids, e.g. immune and
CC inflammatory disorders, platelet disorders, skeletal or bone metabolism
CC disorders, or bone marrow mononuclear disorders, as well as cellular
CC proliferative and/or differentiative disorders, hormonal disorders,
CC neurological disorders, cardiovascular disorders, viral diseases, liver
CC disorders, and pain and metabolic disorders. Conditions that can be
CC treated include cancer, diabetes mellitus, hypothyroidism,
CC hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or
CC viral meningitis, fungal meningoencephalitis, multiple sclerosis,
CC Alzheimer's disease, Parkinson's disease, ataxia-telangiectasia,
CC Huntington's disease, heart failure, angina pectoris, myocardial
CC infarction, rheumatoid arthritis, dermatitis, psoriasis, Crohn's disease,
CC inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host
CC disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The
CC transgenic animals are useful for studying the function and/or activity
CC of a 93870 protein and for identifying and/or evaluating modulators of
CC 93870 activities. The polynucleotides of the invention can be used in
CC gene therapy. This polynucleotide sequence represents the 939 nucleotide
CC DNA of the human G-protein coupled receptor type protein of the invention
SQ Sequence 939 BP; 215 A; 212 C; 205 G; 307 T; 0 U; 0 Other;

Query Match 94.1%; Score 864; DB 6; Length 939;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 914; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAATACCTCCAGGATTCCTCTTGGATCCCTATAGTGACACCCACCTTA 60
DB |||||
QY 25 ATGCTGGCCACAATACCTCCAGGATTCCTCTTGGATCCCTATAGTGACACCCACCTTA 84
DB |||||
QY 61 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGGTGTCATTTCCATTCTTTTC 120
DB |||||
QY 85 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGGTGTCATTTCCATTCTTTTC 144
DB |||||
QY 121 CTCCTGGTGAAAATGAAACCCGGTCAGTGACACCAATGGCGGTGCTATTAACCTGGTGGTG 180
DB |||||
QY 145 CTCCTGGTGAAAATGAAACCCGGTCAGTGACACCAATGGCGGTGCTATTAACCTGGTGGTG 204
DB |||||
QY 181 GTCCACAGCGTCTTCTGTGTGACAGTGCCATTCGCTTGACCTACTCATCAAGAGACT 240
DB |||||
QY 205 GTCCACAGCGTCTTCTGTGTGACAGTGCCATTCGCTTGACCTACTCATCAAGAGACT 264
DB |||||
QY 241 TGGATGTTGGGCTGCGCTCTCTGCAAAATTTGTGAGTGCCATGCTGCACATGCATGATAC 300
DB |||||
QY 265 TGGATGTTGGGCTGCGCTCTCTGCAAAATTTGTGAGTGCCATGCTGCACATGCATGATAC 324
DB |||||

QY 301 CTCACGTTCCCTATTCTATGTGGTGATCCTGGTCAACAGATACCTCATCTCTTCAAGTGC 360
DB |||||
QY 325 CTCACGTTCCCTATTCTATGTGGTGATCCTGGTCAACAGATACCTCATCTCTTCAAGTGC 384
DB |||||
QY 361 AAGACAAAGTGGAAATCTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG 420
DB |||||
QY 385 AAGACAAAGTGGAAATCTACAGAAACTGCATGCTGTGGCTGCCAGTGTGCGCATGTGG 444
DB |||||
QY 421 ACGCTGGTGAATTCATTGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATAGGAA 480
DB |||||
QY 445 ACGCTGGTGAATTCATTGTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATAGGAA 504
DB |||||
QY 481 TACAAATGAGGAGCACTGTTTTTAAATTTCAAAAGAGCTTGCCTTACATATGAAATC 540
DB |||||
QY 505 TACAAATGAGGAGCACTGTTTTTAAATTTCAAAAGAGCTTGCCTTACATATGAAATC 564
DB |||||
QY 541 ATCAACTATATGATAGTAGTCAATTTTGTATAGCCGTGCTGTGATTCCTGTTGGTCTCCAG 600
DB |||||
QY 565 ATCAACTATATGATAGTAGTCAATTTTGTATAGCCGTGCTGTGATTCCTGTTGGTCTCCAG 624
DB |||||
QY 601 GTCTTCATCATATTATGTTGATGGTGCAGAGCTAGCCACTCTTTACTATCCACCAGGAG 660
DB |||||
QY 625 GTCTTCATCATATTATGTTGATGGTGCAGAGCTAGCCACTCTTTACTATCCACCAGGAG 684
DB |||||
QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCCTTGTCTTCTTCTTCCC 720
DB |||||
QY 685 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCCTTGTCTTCTTCTTCCC 744
DB |||||
QY 721 TACAGTCTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAAACG 780
DB |||||
QY 745 TACCAGTCTCTTTAGGATCTATTACTTGAATGTTGTGACGCAATCCAAATGCTGTAGCAGC 804
DB |||||
QY 781 AAGCTTCGATTTTATTAACGAAATCTTCTTCAGTGTAAACAGCAATTAGCTCTATGATTG 840
DB |||||
QY 805 AAGTTGCAATTTTATTAACGAAATCTTCTTCAGTGTAAACAGCAATTAGCTCTATGATTG 864
DB |||||
QY 841 CTTCTCTTTGTCTTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATPAATTTGGCTTATGGAAT 900
DB |||||
QY 865 CTTCTCTTTGTCTTTTGGGGAAGCCATTTGTTTAAAGCAAAAGATPAATTTGGCTTATGGAAT 924
DB |||||
QY 901 TGTGTTTTTGTGCGGT 915
DB |||||
QY 925 TGTGTTTTTGTGCGGT 939
DB |||||

Search completed: April 25, 2004, 18:01:46
Job time : 454 secs

CC derived from the cell, an antibody immunospecific for IGS70. IGS70 is
CC useful for diagnosing a disease or a susceptibility to disease in a
CC subject related to expression or activity of the IGS70 polypeptide in a
CC subject by determining the presence or absence of mutation in the
CC nucleotide sequence encoding IGS70 in the genome of the subject in a
CC sample derived from the subject. IGS70 is also useful identifying agonist
CC or antagonist. The IGS70 protein, polynucleotide, antibody and identified
CC ant/agonists are useful for treating psychiatric and central nervous
CC system (CNS) disorders such as schizophrenia, Alzheimer's disease,
CC multiple sclerosis, anxiety, cardiovascular diseases such as heart
CC failure, angina pectoris, myocardial infarction, kidney disease such as
CC renal failure, gastrointestinal disorders such as irritable bowel
CC syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,
CC inflammation, cancers, asthma, infection (such as bacterial, viral,
CC fungal, protozoal) especially human immunodeficiency virus infection
CC (HIV), diabetes, osteoporosis and allergies. The present sequence encodes
CC the human GPCR IGS70
XX

Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other;

Query Match 94.4%; Score 867; DB 6; Length 1051;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGCGCCACATACCTCCAGGAATTCCTTCGCGATCCTATAGTCACACCCACCTTA 60
Db 60 ATGCTGCGCCACATACCTCCAGGAATTCCTTCGCGATCCTATAGTCACACCCACCTTA 119
QY 61 ATCAGCCCTACTCTCATAGTGTCTTATGCGCGCTGGTGGTGTCTATTTCCATCTTTTC 120
Db 120 ATCAGCCCTACTCTCATAGTGTCTTATGCGCGCTGGTGGTGTCTATTTCCATCTTTTC 179
QY 121 CTCCTGGTGAATAAGAACACCCCGTTCAGTGACACCATGGCGGTCAATTAACCTGGTGTG 180
Db 180 CTCCTGGTGAATAAGAACACCCCGTTCAGTGACACCATGGCGGTCAATTAACCTGGTGTG 239
QY 181 GTCCACAGGTTTCTGCTGACGTGCATTCGCTTGCCTACTCTCATCAGAGACT 240
Db 240 GTCCACAGGTTTCTGCTGACGTGCATTCGCTTGCCTACTCTCATCAGAGACT 299
QY 241 TGGATGTTTGGCTGCCCTTCGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300
Db 300 TGGATGTTTGGCTGCCCTTCGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 359
QY 301 CTCAGTTCTTATCTATGTGTGTATCTGTGTCACAGATACCTCATCTTCTCAAGTGC 360
Db 360 CTCAGTTCTTATCTATGTGTGTATCTGTGTCACAGATACCTCATCTTCTCAAGTGC 419
QY 361 AAAGACAAAGTGGAAATTCACAGAAATCTGATGCTGCGCTGCCAGTGGCATGTGG 420
Db 420 AAAGACAAAGTGGAAATTCACAGAAATCTGATGCTGCGCTGCCAGTGGCATGTGG 479
QY 421 AGCTGGTGATGTGATGTGTGTAACCCCTGGTGTCTCCCGGTATGGAAATCCATGAGAA 480
Db 480 AGCTGGTGATGTGATGTGTGTAACCCCTGGTGTCTCCCGGTATGGAAATCCATGAGAA 539
QY 481 TACATAGGAGACCTGTTTAAATTTCAAGAGAGTTCGTACACATATGTGAAATC 540
Db 540 TACATAGGAGACCTGTTTAAATTTCAAGAGAGTTCGTACACATATGTGAAATC 599
QY 541 ATCAACTATATGATAGTCATTTTGTGATAGCCGTGTGTTGATTCGTGCTTCCAG 600
Db 600 ATCAACTATATGATAGTCATTTTGTGATAGCCGTGTGTTGATTCGTGCTTCCAG 659
QY 601 GTCCTCATCATTTGATGTGTGAGAGCTACCGACTCTTTACTATCCACAGGAG 660
Db 660 GTCCTCATCATTTGATGTGTGAGAGCTACCGACTCTTTACTATCCACAGGAG 719
QY 661 TTCTGGGTTCAGCTGAAACACCTATTTTATAGGGGTGATCTTGTGTTTGTCTTCCC 720
Db 720 TTCTGGGTTCAGCTGAAACACCTATTTTATAGGGGTGATCTTGTGTTTGTCTTCCC 779
QY 721 TACCAGTCTTTAGGATCTATTAATTTGATGATGTTGTGACGCAATCCCAATGCTGTAACAGC 780

Db 780 TACCAGTCTTTAGGATCTATTAATTTGATGATGTTGACGCAATCCATGCTGTAACAGC 839
QY 781 AAGTTGCAATTTATTAACGAATCTCTTGAAGTGAACAGCAATTAAGTCTGCTATGATTTG 840
Db 840 AAGTTGCAATTTATTAACGAATCTCTTGAAGTGAACAGCAATTAAGTCTGCTATGATTTG 899
QY 841 CTCTCTCTTCTCTTCTGGGGGAAGCCATTTGTTTAAAGCAAAAGATAATTTGCTTATGGAAT 900
Db 900 CTCTCTCTTCTCTTCTGGGGGAAGCCATTTGTTTAAAGCAAAAGATAATTTGCTTATGGAAT 959
QY 901 TGTGTTTGTGCGCTTAG 918
Db 960 TGTGTTTGTGCGCTTAG 977

RESULT 14

AAL53413

ID AAL53413 standard; cDNA; 1684 BP.

XX AAL53413;

XX 12-DEC-2002 (first entry)

XX 1684 nt cDNA of human G-protein coupled receptor type protein.

XX Anti-HIV; cytostatic; antidiabetic; antiaesthetic; antiinflammatory;
XX haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic;
XX antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;
XX cardiac; dermatological; antifertility; hepatotropic; antiallergic;
XX antipariatic; ophthalmological; antianginal; antithyroid; anticonvulsant;
XX antirheumatic; antiarthritic; G-protein coupled receptor; subfamily 1;
XX 93870 receptor; immune; inflammatory disorder; platelet disorder;
XX skeletal; bone metabolism disorder; bone marrow mononuclear disorder;
XX cellular proliferative; differentiative disorder; hormonal disorder;
XX neurological disorder; cardiovascular disorder; viral disease; pain;
XX liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;
XX hypothyroidism; hyperthyroidism; reproductive; fertility disorder; HIV;
XX Alzheimer's disease; Parkinson's disease; ataxia-telangiectasia;
XX Huntington's disease; heart failure; angina pectoris; dermatitis;
XX myocardial infarction; rheumatoid arthritis; psoriasis; Crohn's disease;
XX inflammatory bowel disease; asthma; graft-versus-host disease; allergy;
XX conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy;
XX transgenic animal; human; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 147..1088

XX /*tag= a

XX /product= "Human G-protein coupled receptor type protein

XX 93870"

XX WO200270657-A2.

XX 12-SEP-2002.

XX 28-FEB-2002; 2002WO-US0006455.

XX 01-MAR-2001; 2001US-0272677P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Glucksmann MA;

XX WPI; 2002-732793/79.

XX P-PSDB; AAO22919.

XX New G-protein coupled receptor used in receptor assays as a target for
XX diagnosis and treatment of receptor-mediated disorders, e.g. immune and
XX inflammatory disorders, platelet disorders, skeletal or bone metabolism
XX disorders.

PI Nguyen DB, Lee EA, Lu DAM, Ison CH, Walsh RT, Policky JL;
XX WPI; 2002-426012/45.
DR P-PSDB; AAE23414.
XX Novel G-protein coupled receptor polypeptides referred as GCREC peptides,
PT useful for treating multiple sclerosis, cholecystitis heart failure,
PT angina pectoris, rheumatoid arthritis, obesity, osteoporosis.
XX Claim 83; Page 140; 147pp; English.
XX The invention relates to human G-protein coupled receptor (GCREC 1-16)
CC polypeptides and polynucleotides. Sequences of the invention are useful
CC for the diagnosis, treatment and prevention of cell proliferative (e.g.
CC cancer, cirrhosis), neurological (e.g. multiple sclerosis, Huntington's
CC disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris,
CC heart failure), gastrointestinal (e.g. anorexia, cholecystitis),
CC autoimmune/inflammatory (rheumatoid arthritis, Hashimoto's thyroiditis)
CC and metabolic disorders (e.g. obesity, osteoporosis), viral infections,
CC atherosclerosis and hepatitis. GCREC proteins are useful for identifying
CC compounds that modulate, mimic and block olfactory and taste sensations.
CC They are also useful for identifying GCREC modulators. GCREC DNAs are
CC useful in gene therapy. The present sequence is human GCREC-6 cDNA
XX SQ Sequence 1499 BP; 375 A; 340 C; 329 G; 455 T; 0 U; 0 Other;
Query Match 96.6%; Score 887; DB 6; Length 1499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGGGCAATACCTCCAGGAATTCCTTGGGATCCCTATAGTGACACCCACTTA 60
DB 381 ATGCTGGGCAATACCTCCAGGAATTCCTTGGGATCCCTATAGTGACACCCACTTA 440
QY 61 ATCAGGCTCTACTTCATAGTGTCTTATGGGGCTGGTGGTGTCTATTTCCATCTTTTC 120
DB 441 ATCAGGCTCTACTTCATAGTGTCTTATGGGGCTGGTGGTGTCTATTTCCATCTTTTC 500
QY 121 CTCCTGGTGAATAGAACCCCGTCAGTGACACCATGCGGTCAATTAACCTGGTGTG 180
DB 501 CTCCTGGTGAATAGAACCCCGTCAGTGACACCATGCGGTCAATTAACCTGGTGTG 560
QY 181 GTCCACAGCGTTTCTGCTGACAGTGCCATTTGCTTACCTACCTCATCAAGAGACT 240
DB 561 GTCCACAGCGTTTCTGCTGACAGTGCCATTTGCTTACCTACCTCATCAAGAGACT 620
QY 241 TGGATGTTGGGTGCGCTTCTCAAAATTTGTGAGTGCCATGTGCATCCACATGTAC 300
DB 621 TGGATGTTGGGTGCGCTTCTCAAAATTTGTGAGTGCCATGTGCATCCACATGTAC 680
QY 301 CTCACGTTCTTATCTATGTGTGATCCCTGGTCAACGATACCTCATCTTCAAGTGC 360
DB 681 CTCACGTTCTTATCTATGTGTGATCCCTGGTCAACGATACCTCATCTTCAAGTGC 740
QY 361 AAAGACAAAGTGAATTTCTACAGAAATCTGATGCTGTGGTCCAGTCTGCGATGTGG 420
DB 741 AAAGACAAAGTGAATTTCTACAGAAATCTGATGCTGTGGTCCAGTCTGCGATGTGG 800
QY 421 ACCTGGTGATTTCTGATTTGGTACCCCTGGTGTCTCCGGTATGGAATCCAGGAA 480
DB 801 ACCTGGTGATTTCTGATTTGGTACCCCTGGTGTCTCCGGTATGGAATCCAGGAA 860
QY 481 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTTCACATATGTGAAATC 540
DB 861 TACAATGAGGAGCAGCTGTTTAAATTTCAAAAGAGCTTGTTCACATATGTGAAATC 920
QY 541 ATCAACTATATAGTATCATTTTGTGATGATCCGCTGTGATCTGTGTTCTTCCAG 600
DB 921 ATCAACTATATAGTATCATTTTGTGATGATCCGCTGTGATCTGTGTTCTTCCAG 980
QY 601 GTCTTCATCATATGTTGATGGTGCAAGACTAGCCACTCTTTACTATCCACACAGGAG 660
DB 981 GTCTTCATCATATGTTGATGGTGCAAGACTAGCCACTCTTTACTATCCACACAGGAG 1040

QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTACCTCTGTTTCTTCCCTCCC 720
DB 1041 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTACCTCTGTTTCTTCCCTCCC 1100
QY 721 TACCAGTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCATGCTGTAAACAGC 780
DB 1101 TACCAGTCTTTTAGGATCTATTACTTGAATGTTGTGACGCAATTCATGCTGTAAACAGC 1160
QY 781 AAGTTGCTATTTTATAAGAAATCTTCTTGAGTGTACACGAATTAGCTGCTATGATTG 840
DB 1161 AAGTTGCTATTTTATAAGAAATCTTCTTGAGTGTACACGAATTAGCTGCTATGATTG 1220
QY 841 CTCTCTTTTGTCTTTGGGGGAAGCAATTTGTTTAAAGCAAAAGATAAT 887
DB 1221 CTCTCTTTTGTCTTTGGGGGAAGCAATTTGTTTAAAGCAAAAGATAAT 1267
RESULT 13
ABK87351
ID ABK87351 standard; cDNA; 1051 BP.
XX AC ABK87351;
XX DT 24-SEP-2002 (first entry)
XX Human cDNA encoding G protein-coupled receptor IGS70.
DE Human; ss; Gene; G protein-coupled receptor; GPCR; IGS70; CNS;
KW psychiatric disorder; central nervous system disorder; schizophrenia;
KW Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;
KW heart failure; angina pectoris; myocardial infarction; kidney disease;
KW renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;
KW inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;
KW asthma; infection; human immunodeficiency virus infection; HIV; diabetes;
KW osteoporosis; allergy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 60..977
FT /tag= a
FT /product= "GPCR IGS70"
XX WO200244212-A2.
XX PD 06-JUN-2002.
XX PF 23-NOV-2001; 2001WO-EP013706.
XX PR 30-NOV-2000; 2000EP-00204280.
XX PR 05-DEC-2000; 2000US-0251045P.
XX PA (SOLV) SOLVAY PHARM BV.
XX PI Deleersnijder W, Blockx H, De Moor L;
XX WPI; 2002-527703/56.
XX P-PSDB; AAU99179.
XX Novel G-protein coupled receptor IGS70 polypeptide useful for treating
PT dysfunctions, disorders or disease related to lung, bone marrow, spinal
PT cord immune system.
XX Claim 1; Page 6; 58pp; English.
XX The invention relates to a G protein-coupled receptor (GPCR) IGS70
CC polypeptide including sequences that are 98-99.6% identical. Also
CC included are the polynucleotide encoding IGS70 (including sequences 98-
CC 99.6% identical to the polynucleotide or the DNA insert contained in
CC plasmid CBS 109818), a hybridisation probe derived from the
CC polynucleotide, a DNA or RNA expression system producing IGS70, a host
CC comprising the expression system, IGS70 receptor membrane preparation


```
XX
PD 02-JAN-2003.
XX
XX 18-JUN-2002; 2002EP-00013517.
PF
XX
XX 18-JUN-2001; 2001JP-00246789.
PR
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
PI WPI; 2003-315783/31.
XX
XX P-PSDB; ADC86555.
DR
XX
XX New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 1; SEQ ID NO 1007; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
CC invention.
XX
XX Sequence 113306 BP; 34476 A; 21483 C; 21391 G; 35956 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 918; DB 9; Length 113306;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGCGCCCAATACCTCCAGGAATTCCTCTCGGATCTATAGTGACACCCACCTTA 60
DB 11540 ATGCTGCGCCCAATACCTCCAGGAATTCCTCTCGGATCTATAGTGACACCCACCTTA 11599
QY 61 ATCAGCCCTTACTTCATAGTGCTTATTGCGGGCTGGTGGGTGATTCATTCATTCCTTTTC 120
DB 11600 ATCAGCCCTTACTTCATAGTGCTTATTGCGGGCTGGTGGGTGATTCATTCATTCCTTTTC 11659
QY 121 CTCCTGGTGAATTAACACCCGGTCAGTGACCCACCATGGGGTCAATTAATTCGTTGGTGG 180
DB 11660 CTCCTGGTGAATTAACACCCGGTCAGTGACCCACCATGGGGTCAATTAATTCGTTGGTGG 11719
QY 181 GTCCACAGCGTTTCTGTGACAGTGCCATTTCCCTTGACCTTACCTCATCAAGAAGACT 240
DB 11720 GTCCACAGCGTTTCTGTGACAGTGCCATTTCCCTTGACCTTACCTCATCAAGAAGACT 11779
QY 241 TGGATGTTGGGCTGCCCTTCTGAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 300
DB 11780 TGGATGTTGGGCTGCCCTTCTGAAATTTGTAGTGCCATGCTGCACATCCACATGTAC 11839
QY 301 CTCAGGTTCTTATTCTATGTGTGATCTGTGTCACAGATACCTCATCTTCTCAAGTGC 360
DB 11840 CTCAGGTTCTTATTCTATGTGTGATCTGTGTCACAGATACCTCATCTTCTCAAGTGC 11899
QY 361 AAAGCAAAAGTGGAAATTCACAGAAAATGATGCTGTGGCTGGCAGTGGCATGTGG 420
DB 11900 AAAGCAAAAGTGGAAATTCACAGAAAATGATGCTGTGGCTGGCAGTGGCATGTGG 11959
QY 421 ACGCTGGTGATTTGATGTTGTGATCCCTCGTGTGTTGCTCCCGTATGGAATCCATGAGAA 480
DB 11960 ACGCTGGTGATTTGATGTTGTGATCCCTCGTGTGTTGCTCCCGTATGGAATCCATGAGAA 12019
QY 481 TACATGAGGAGCACTGTTTAAATTTACAAAGAGCTTGCTTACACATATGTGAAATC 540
DB 12020 TACATGAGGAGCACTGTTTAAATTTACAAAGAGCTTGCTTACACATATGTGAAATC 12079
QY 541 ATCAACTATATGATAGTCAATTTTGTGTCATAGCCGTTGCTGTGATTCCTGGTCTTCCAG 600
```

```
DB 12080 ATCAACTATATGATAGTCAATTTTGTGTCATAGCGTTGCTGTGATTCCTGGTCTTCCAG 12139
QY 601 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTACTATATCCACAGGAG 660
DB 12140 GTCTTCATCATTTATGTTGATGTCAGAGCTACGCCACTCTTTACTATATCCACAGGAG 12199
QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCTTCCC 720
DB 12200 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTTGTGTTTCTTCCC 12259
QY 721 TACAGTTCCTTTAGGATCTATTACTTGAATGTTGTGACGATTCGAATCGCTGTATACAG 780
DB 12260 TACAGTTCCTTTAGGATCTATTACTTGAATGTTGTGACGATTCGAATCGCTGTATACAG 12319
QY 781 AAGTGTGATTTTATAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGCTATGATTG 840
DB 12320 AAGTGTGATTTTATAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGCTATGATTG 12379
QY 841 CTCTCTCTTCTCTTTGCGGGAAGCCATTTGTTTAAACAAAAGATAATTCGCTTATGGAAT 900
DB 12380 CTCTCTCTTCTCTTTGCGGGAAGCCATTTGTTTAAACAAAAGATAATTCGCTTATGGAAT 12439
QY 901 TGTGTTTGTGCGGTTAG 918
DB 12440 TGTGTTTGTGCGGTTAG 12457
RESULT 12
AAD37670
ID AAD37670 standard; cDNA; 1499 BP.
XX
AC AAD37670;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human G-protein coupled receptor-6 (GCRC-6) cDNA.
XX
KW Human; G-protein coupled receptor-6; GCRC-6; atherosclerosis; cancer;
KW cell proliferative disorder; gastrointestinal; autoimmune; metabolic;
KW neurological; inflammatory; cardiovascular; viral infection; anorexia;
KW cirrhosis; multiple sclerosis; Huntington's disease; gene therapy;
KW Alzheimer's disease; heart failure; hepatitis; cholecystitis; obesity;
KW rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris;
KW osteoporosis; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 381..1400
FT /tag= a
FT /product= "Human GCRC-6 protein"
XX
XX WO200226825-A2.
XX
XX 04-APR-2002.
XX
XX 28-SEP-2001; 2001WO-US030661.
XX
XX 29-SEP-2000; 2000US-0236546P.
XX 13-OCT-2000; 2000US-0240589P.
XX 20-OCT-2000; 2000US-0242223P.
XX 20-OCT-2000; 2000US-0242322P.
XX 03-NOV-2000; 2000US-0245855P.
XX 03-NOV-2000; 2000US-0245900P.
XX 09-NOV-2000; 2000US-0247587P.
XX 15-NOV-2000; 2000US-0249343P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Baughn MR, Graul RC, Walia NK, Gandhi AR, Hafalia AJA;
XX Rankumar J, Tribouley CM, Thornton M, Kallick DA, Yao MG;
XX Elliott VS, Burford N, Khan FA, Yue H, Lu Y, Arvizu C, Roopa R;
```


XX Human; gene; ds; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
KW nG protein coupled receptor; communication; serpentine structure;
KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;
KW genetic predisposition; brain; immune response; gene therapy;
KW anxiety disorder; depression; bipolar disorder; schizophrenia;
KW Huntington's disease; dyskinesia; manic depression; stroke;
KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
KW tranquiliser.

XX Homo sapiens.
OS
XX WO200264789-A1.
XX
XX 22-AUG-2002.
XX
XX 14-FEB-2001; 2001WO-US004641.
XX
XX 14-FEB-2001; 2001WO-US004641.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Lind P, Parodi LA, Vogeli G, Wood LS;
XX
XX WPI; 2002-674879/72.
XX
XX P-PSDB; ABG93787.

XX New nucleic acids and polypeptides of the nG protein-coupled receptor,
PT useful for treating or diagnosing a mental disorder or a disorder
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
PT Parkinson's disease.

XX Example 1; Page 84-85; 244pp; English.

XX The invention discloses an isolated human polypeptide, and encoding the
CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly
CC nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
CC communication between cells and their environment and are characterised
CC by a serpentine structure that passes through the cell membrane seven
CC times, hence the reason such receptors are sometimes called seven
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
CC useful for identifying an nGPCR allelic variant that correlates with a
CC mental disorder, for isolating an antibody that binds to an epitope of
CC the polypeptide, for identifying a compound that binds to the polypeptide or
CC polynucleotide and/or modulates its biological activity, for screening a
CC human subject to diagnose a disorder, or a genetic predisposition to a
CC disorder, affecting the brain or a genetic disposition to the disorder,
CC for identifying compounds useful for the treatment of a mental disorder
CC and for identifying a compound useful as a modulator of binding between
CC nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also
CC useful for inducing an immune response in a mammal. The nucleic acid or
CC polypeptide is particularly useful, using gene therapy, for treating e.g.
CC anxiety disorders, depression, bipolar disorder, schizophrenia,
CC Huntington's disease, dyskinesia, manic depression, stroke, Parkinson's
CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
CC be used for treating diabetes, inflammation or wounds. The sequences
CC presented in ABS70202-ABS70248, ABS70338 and ABS70243 are the DNAs
CC encoding the nGPCRs (also referred to as beGPCRs)

XX Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 918; DB 6; Length 2525;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCCACAACTACCTCCAGGAATTCCTTGGATCCTATAGTACACCCCACTTA 60
DB 27 ATGCTGGCCACAACTACCTCCAGGAATTCCTTGGATCCTATAGTACACCCCACTTA 86
QY 61 ATCAGCCTCTACTTCATAGTGGTATTTGGCGGCTGGTGGTGTCAATTCATTTTTC 120
DB 87 ATCAGCCTCTACTTCATAGTGGTATTTGGCGGCTGGTGGTGTCAATTCATTTTTC 146

QY 121 CTCCTGGTGAATGAACACCCGGTCAGTGACCAACATGGCGGTCAATTAACCTTGGTGGTG 180
DB 147 CTCCTGGTGAATGAACACCCGGTCAGTGACCAACATGGCGGTCAATTAACCTTGGTGGTG 206
QY 181 GTCACAGAGCTTTTCTGCTGACAGTGCCATTTTGGCTTGACCTACCTCATCAAGAGACT 240
DB 207 GTCCACAGAGCTTTTCTGCTGACAGTGCCATTTTGGCTTGACCTACCTCATCAAGAGACT 266
QY 241 TGGATGTTTGGGCTGCCCTTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCCATGTAC 300
DB 267 TGGATGTTTGGGCTGCCCTTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCCATGTAC 326
QY 301 CTCAGCTTCTATTTCTATGTTGGTGATCCTGGTCACAGATACCTCATCTTCTTCAAGTGC 360
DB 327 CTCAGCTTCTATTTCTATGTTGGTGATCCTGGTCACAGATACCTCATCTTCTTCAAGTGC 386
QY 361 AAAGACAAAGTGAATTTCTACAGAAAACCTGCATGCTGTGGCTGCCAGTGGCATGTGG 420
DB 387 AAAGACAAAGTGAATTTCTACAGAAAACCTGCATGCTGTGGCTGCCAGTGGCATGTGG 446
QY 421 ACGCTGGTGAATTTCTATGTTGGTGATCCTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 480
DB 447 ACGCTGGTGAATTTCTATGTTGGTGATCCTGGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGAA 506
QY 481 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 540
DB 507 TACAATGAGGAGCACTGTTTAAATTTTCAAAAGAGCTTGTCTTACACATATGTGAAAATC 566
QY 541 ATCAACTATATGATGATGATTTTGTGATAGCCGCTTGTGATTTCTGTTGGTCTTCCAG 600
DB 567 ATCAACTATATGATGATGATTTTGTGATAGCCGCTTGTGATTTCTGTTGGTCTTCCAG 626
QY 601 GTCTTTCATCATTTATGTTGATGTTGTCAGAGAGCTACGCCACTCTTTACTATCCACAGGAG 660
DB 627 GTCTTTCATCATTTATGTTGATGTTGTCAGAGAGCTACGCCACTCTTTACTATCCACAGGAG 686
QY 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTGCATCTTGTGTTTCTTCTTCCC 720
DB 687 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGTGCATCTTGTGTTTCTTCTTCCC 746
QY 721 TACAGTTCTTTAGGATCTATCTTGAATGTTGTCAGGATTCCTCAATGCTGTGAACAGC 780
DB 747 TACAGTTCTTTAGGATCTATCTTGAATGTTGTCAGGATTCCTCAATGCTGTGAACAGC 806
QY 781 AAGTTTGCATTTTATAACGAATCTTCTTGAAGTGTAAACAGCAATTAGCTGTATGATTG 840
DB 807 AAGTTTGCATTTTATAACGAATCTTCTTGAAGTGTAAACAGCAATTAGCTGTATGATTG 866
QY 841 CTCTCTTTGCTTTGGGGAGGAGCATTTGTTTAAAGCAAGAGATAATGGCTTATGGAAT 900
DB 867 CTCTCTTTGCTTTGGGGAGGAGCATTTGTTTAAAGCAAGAGATAATGGCTTATGGAAT 926
QY 901 TGTGTTTGTGCCGTTAG 918
DB 927 TGTGTTTGTGCCGTTAG 944

RESULT 11

ADC86554
ID ADC86554 standard; DNA; 113306 BP.

XX ADC86554;

XX AC ADC86554;

XX DT 01-JAN-2004 (first entry)

XX DE Human GPCR gene SEQ ID NO:1007.

XX ds; gene; human; GPCR;

XX KW guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX OS Homo sapiens.

XX XX EP1270724-A2.

PN

neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder; attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; ds.

Homo sapiens.

WO200136473-A2.

25-MAY-2001.

16-NOV-2000: 2000WO-US031581.

16-NOV-1999: 99US-0165838P.

17-NOV-1999; 99US-016607IP.
19-NOV-1999; 99US-0166678P

28-DEC-1999; 99US-0173396P.
22-FEB-2000; 2000US-0184129P.

28-FEB-2000; 2000US-0185421P.

02-MAR-2000; 2000US-0186530P.

09-MAR-2000; 2000US-0188114P.

21-MAR-2000; 2000US-0190800P.

02-MAY-2000; 2000US-0201190P.

25-MAY-2000; 2000US-0207094P.

(PHAA) PHARMACIA & UPJOHN CO

Vogeli G, Wood LS, Parodi L

СПЕЛТІІ НА, НАУЛЕВ КЗ, ВАП

WPL; 2001-389826/41.
P-PSDB: AAG80969.

New C protein-coupled receptor

useful for diagnosing and tre

Claim 4; Page 89-90; 261pp; E

The present invention relates

31-38, 40, 41, 53-60) and their coding sequences. The present sequences

also known as seven transmembrane receptors and function in signal

human to diagnose a

identifying compo

disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,

diseases, proliferative disorders and hormonal disorders

including schizophrenia, ADHD/ADD (a

disorders, infection, genetic disorders, and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.

Sequence 2525 BP; 700 A; 510 C; 501 G; 814 T; 0 U; 0 Other;

100.0%: Score 918; DB 4; Length 2525;

Best Local Similarity 100.0%; PRed: NO: 0; Mismatches 0: Mismatches

1 ATGCGCTGGCCACCAATACCTCCAGGAATTCCCTCTTGCGATCCTATAGTGACACCCCACTTA 60

Db	27	ATGCCCTGGCCCAAAATACCTCTCCAGGAATTCCTCTTGGCATCCCTATAGTAGACACCCCACTTA	86
Qy	61	ATCAGCCTCTACTTCATAGTGCCTTATATGGCGGCTGGTGGGTGTCAATTTCCATCTCTTTTC	120
Db	87	ATCAGCCTCTACTTCATAGTGCCTTATATGGCGGCTGGTGGGTGTCAATTTCCATCTCTTTTC	146
Qy	121	CTCCTCGTGGAAATGAACACCCGGTCAGTAGACACCATGGCGGTCAATTAACCTTGGTGGTG	180
Db	147	CTCTCTGGTGNAAATGAACACCCGGTCAGTAGACACCATGGCGGTCAATTAACCTTGGTGGTG	206
Qy	181	GTCACAGCGTTTTTCTGTGTGACAGTGCCATTTGCGCTTGACCTTACCTCATCAAGAAGACT	240
Db	207	GTCACAGCGTTTTTCTGTGTGACAGTGCCATTTGCGCTTGACCTTACCTCATCAAGAAGACT	266
Qy	241	TGAGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGTGTGACATCCACATGTAC	300
Db	267	TGAGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGTGTGACATCCACATGTAC	326
Qy	301	CTCACGTTCTCTATATGTTGTTGATCTCTGGTGCACAGATACCTCATCTTCTTCCAGTGC	360
Db	327	CTCACGTTCTCTATATGTTGTTGATCTCTGGTGCACAGATACCTCATCTTCTTCCAGTGC	386
Qy	361	AAAGACAAAGTGGAAATTCACAGAAAACATGCATCTGTGGCTGCCAGTGTGCGCATGTGG	420
Db	387	AAAGACAAAGTGGAAATTCACAGAAAACATGCATCTGTGGCTGCCAGTGTGCGCATGTGG	446
Qy	421	ACGCTGGTGTATGTCTCATTTGTGTGTACCCCTGGTTGTCTCCCGTATGGAATCCATGAGAA	480
Db	447	ACGCTGGTGTATGTCTCATTTGTGTGTGTACCCCTGGTTGTCTCCCGTATGGAATCCATGAGAA	506
Qy	481	TACAAATGAGGAGCACTGTTTTAAATTTCAAAAAGAGCTTGCTTTACACATATGTGAAAATC	540
Db	507	TACAAATGAGGAGCACTGTTTTAAATTTCAAAAAGAGCTTGCTTTACACATATGTGAAAATC	566
Qy	541	ATCAACTATATGATAGTCAATTTTGTGTGTATAGCCGTTGTGTGTATCTCTGTGGTCTTCCAG	600
Db	567	ATCAACTATATGATAGTCAATTTTGTGTGTGTATAGCCGTTGTGTGTATCTCTGTGGTCTTCCAG	626
Qy	601	GTCTTCAATCAATATGTTGATGGTGCAGAGACTACGCCACTCTTTTACTATCCCAACCAGGAG	660
Db	627	GTCTTCAATCAATATGTTGATGGTGCAGAGACTACGCCACTCTTTTACTATCCCAACCAGGAG	686
Qy	661	TTCTGGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTATCCCTGTTGTTTCCCTTCCC	720
Db	687	TTCTGGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTATCCCTGTTGTTTCCCTTCCC	746
Qy	721	TACCAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGCATTTCCAAATGCTGTAAACGC	780
Db	747	TACCAGTTCCTTAGGATCTATTACTTGAATGTTGTGACGCATTTCCAAATGCTGTAAACGC	806
Qy	781	AAGTTGCAATTTTATACGAAATCTTCTCTGAGTGTAAACAGCAATTAGCTGCTATGATTG	840
Db	807	AAGTTGCAATTTTATACGAAATCTTCTCTGAGTGTAAACAGCAATTAGCTGCTATGATTG	866
Qy	841	CTTCTCTTCTCTTTTGGGGAGCCATTTGTTTTAAGCAAAAGATAATTTGGCTTATGGAAT	900
Db	867	CTTCTCTTCTCTTTTGGGGAGCCATTTGTTTTAAGCAAAAGATAATTTGGCTTATGGAAT	926
Qy	901	TGTGTTTTGTGCGGTAG	918
Db	927	TGTGTTTTGTGCGGTAG	944

RESULT 10

RESUL TO
ABS70242

ABS70242
ID ABS70242 standard; DNA; 2525 BP.

XX ARS70242:

26-NOV-2002 (first entry)

DE DNA encoding human G protein-coupled receptor, nGPCR-16.

XX	19-NOV-2002 (first entry)
DT	
DE	Human GCREC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54.
XX	
DE	GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
XX	CYTOSTATIC; neuroprotective; antiparkinsonian; hepatotropic; laxative;
KW	cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
KW	cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;
KW	prozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
KW	Parkinson's disease; Crohn's disease; constipation; infection;
KW	gene therapy; Gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200263004-A2.
XX	
PD	15-AUG-2002.
XX	
PF	06-FEB-2002; 2002WO-US003635.
XX	
XX	07-FEB-2001; 2001US-0267322P.
PR	23-FEB-2001; 2001US-0271215P.
PR	08-MAR-2001; 2001US-0274551P.
PR	23-MAR-2001; 2001US-0278507P.
PR	30-MAR-2001; 2001US-0280597P.
PR	02-APR-2001; 2001US-0281107P.
PR	06-APR-2001; 2001US-0281212P.
XX	
XX	(INCY-) INCYTE GENOMICS INC.
XX	
PA	Baughn MR, Tribunoy CM, Nguyen DB, Thornton M, Yao MG;
PI	Kallick DA, Gandhi AR, Wallia NK, Arvizu C, Elliott VS, Hafalia AJA;
PI	Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Buford N, Lu DAM;
PI	Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
PI	Warren BA, Yang J, Lee EA, Harland L;
XX	
DR	WPI; 2002-627557/67.
XX	P-PSDB; AAB711327.
XX	
PT	New human G-protein coupled receptors (GCREC), useful for diagnosing or
PT	treating a disease or condition associated with decreased expression or
PT	over expression of functional GCRECs e.g. cancer, Alzheimer's and
PT	Parkinson's.
XX	
PS	Claim 115; Page 213-214; 239pp; English.
XX	
PS	This invention describes novel polypeptides which have anti-HIV,
CC	antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,
CC	hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,
CC	antibacterial, fungicide and protozoacide activity. The products of the
CC	invention are useful for treating a disease or condition associated with
CC	decreased expression or over expression of functional G-protein coupled
CC	receptors (GCREC), while antibodies generated against the polypeptide of
CC	the invention are useful for diagnosing a condition or disease associated
CC	with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,
CC	stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
CC	constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
CC	The compounds described in the invention can be used for gene therapy.
CC	AAB7580-AAB78627 encode the GCREC proteins represented by AAB71322-
CC	AAB71369, described in the disclosure of the invention
XX	
XX	Sequence 1460 BP; 363 A; 327 C; 316 G; 454 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 918; DB 6; Length 1460;
Best Local Similarity	100.0%; Pred. No. 0;
Matches	918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGCCTGGCCAAATACCTCCAGGATTCCTCTTGGCATCTCTATAGTGACACCCCACTTA 60
DB	343 ATGCCTGGCCAAATACCTCCAGGATTCCTCTTGGCATCTCTATAGTGACACCCCACTTA 402
QY	61 ATCAGCCTCTACTTTCATAGTGTCTTATGCGGGGTGGTGGGTGCATTTCATTCTTTTC 120

QY 781 AAGTTGCAATTTTATACGAATCTCTTGGAGTGAACGCAATAGCTGCTATGATTG 840
DB |||||
QY 781 AAGTTGCAATTTTATACGAATCTCTTGGAGTGAACGCAATAGCTGCTATGATTG 840
DB |||||
QY 841 CTTCTCTTTGCTCTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
DB |||||
QY 841 CTTCTCTTTGCTCTTTGGGGAAGCCATTGGTTTAAAGCAAAAGATAATTTGGCTTATGGAAT 900
DB |||||
QY 901 TGTGTTTTGCGGTAG 918
DB |||||
QY 901 TGTGTTTTGCGGTAG 918
DB |||||

RESULT 6

AAF88583

ID AAF88583 standard; cDNA; 1336 BP.

AC

AAF88583;

XX

DT 19-NOV-2002 (first entry)

XX

DE Human GREC-4 cDNA INCYTE ID 90012430CD1 SEQ ID 52.

XX

KW GREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
cystostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;
KX protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
KW Parkinson's disease; Crohn's disease; constipation; infection;
KW Gene therapy; Gene; ss.

XX

OS Homo sapiens.

XX

PN WO200263004-A2.

XX

PD 15-AUG-2002.

XX

PF 06-FEB-2002; 2002WO-US003635.

XX

PR 07-FEB-2001; 2001US-0267322P.

XX

PR 23-FEB-2001; 2001US-0271215P.

XX

PR 08-MAR-2001; 2001US-0274551P.

XX

PR 23-MAR-2001; 2001US-0278507P.

XX

PR 30-MAR-2001; 2001US-0280597P.

XX

PR 02-APR-2001; 2001US-0281107P.

XX

PR 06-APR-2001; 2001US-0282121P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Baughn MR, Triboulevy CM, Nguyen DB, Thornton M, Yao MG;
PI Kallick DA, Gandhi AR, Walia NK, Arvizu C, Elliott VS, Hafalia AJA;
PI Ramkumar J, Fei J, Tang YF, Yue H, Reddy R, Butford N, Lu DAM;
PI Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
PI Warren BA, Yang J, Lee EA, Harland L;

XX

DR WPI: 2002-627557/67.

XX

DR P-PSDB; AAB71325.

XX

XX New human G-protein coupled receptors (GREC), useful for diagnosing or
PT treating a disease or condition associated with decreased expression or
PT over expression of functional GRECs e.g. cancer, Alzheimer's and
PT Parkinson's.

XX

PS Claim 113; Page 212-213; 239pp; English.

XX

CC This invention describes novel polypeptides which have anti-HIV,
antiarteriosclerotic, cyrostatic, neuroprotective, antiparkinsonian,
CC hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,
CC antibacterial, fungicide and protozoacide activity. The products of the
CC invention are useful for treating a disease or condition associated with
decreased expression or over expression of functional G-protein coupled
CC receptors (GREC), while antibodies generated against the polypeptide of
CC the invention are useful for diagnosing a condition or disease associated
CC with the expression of GREC e.g. arteriosclerosis, cirrhosis, cancer,

QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCC 720
 Db 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCC 720
 QY 721 TACCAAGTTCTTAGCATCTATTAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGCTATGTTG 840
 Db 721 TACCAAGTTCTTAGCATCTATTAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGCTATGTTG 840
 QY 781 AAGGTTGCAATTTTAAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGCTATGTTG 840
 Db 781 AAGGTTGCAATTTTAAACGAAATCTTCTTGAGTGTAAACAGCAATAGCTGCTATGTTG 840
 QY 841 CTCTCTTTGCTTTGGGGAGGCAATGCTGTTAGGCAAAAGATAATGGCTTATGGAAT 900
 Db 841 CTCTCTTTGCTTTGGGGAGGCAATGCTGTTAGGCAAAAGATAATGGCTTATGGAAT 900
 QY 901 TGTGTTTGTGCGGTAG 918
 Db 901 TGTGTTTGTGCGGTAG 918

RESULT 5
 AAL57070
 ID AAL57070 standard; DNA; 1040 BP.
 AC AAL57070;
 XX
 DT 17-SEP-2003 (first entry)
 XX Human G-protein coupled receptor GAVE18 DNA sequence.
 DE
 KW Human G-protein coupled receptor; GAVE18; signal transduction;
 KW inflammation; physiological immunological response; anti-inflammatory;
 KW antiasthmatic; antirheumatic; antiarthritic; antisense therapy;
 KW chromosomal mapping; tissue typing; forensic biology;
 KW predictive medicine; asthma; chronic obstructive pulmonary disease; COPD;
 KW rheumatoid arthritis; gene; ds.
 XX Homo sapiens.
 OS

Key Location/Qualifiers
 CDS 1..918
 FT /*tag= a
 FT /product= "GAVE18 protein"
 XX
 WO2003042399-A2.
 XX
 PD 22-MAY-2003.
 XX
 XX 08-NOV-2002; 2002WO-US035887.
 XX
 XX 13-NOV-2001; 2001US-0354150P.
 PR 22-MAR-2002; 2002GB-00006891.
 XX
 XX (AVET) AVENTIS PHARM INC.
 FA
 XX
 XX Bishindrello H, Cai J, Busch SJ, Gassenhuber J;
 XX
 XX WPI; 2003-457496/43.
 DR P-PSDB; RAO27265.
 DR
 XX
 PT New GAVE18 polypeptide and nucleic acid molecule encoding the
 PT polypeptide, useful for preventing and treating a disease or disorder
 PT associated with aberrant expression or activity of GAVE18, e.g. asthma or
 PT rheumatoid arthritis.
 XX
 XX Claim 1; Fig 5; 88pp; English.
 PS
 XX
 CC This invention relates to a novel G-protein coupled receptor (GAVE18)
 CC that is involved in signal transduction in respect to inflammation and
 CC the physiological immunological response. Molecules which may modulate
 CC the signalling activity or signal transduction of the receptor may be

CC antiinflammatory, antiasthmatic, antirheumatic or antiarthritic. The
 CC GAVE18 receptor and the DNA sequence encoding it may be a target for
 CC antisense therapy or gene therapy. The nucleic acid molecule, GAVE18
 CC proteins and antibodies may be useful in screening assays, detection
 CC assays (for example chromosomal mapping, tissue typing or forensic
 CC biology), or predictive medicine (for example diagnostic assays;
 CC prognostic assays, monitoring clinical trials and pharmacogenomics. The
 CC nucleic acid molecule, GAVE18, anti-GAVE18 antibodies, agonist, inverse
 CC agonist and antagonist are also useful for preventing and treating a
 CC disease or disorder associated with aberrant expression or activity of
 CC GAVE18, such as inflammation and immunological-related diseases or
 CC disorders, for example asthma, chronic obstructive pulmonary disease or
 CC rheumatoid arthritis. The present sequence is the DNA sequence encoding
 CC the GAVE18 protein of the invention
 XX

SQ Sequence 1040 BP; 289 A; 216 C; 213 G; 322 T; 0 U; 0 Other;
 Query Match 100.0%; Score 918; DB 8; Length 1040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTTATAGTGACACCCCACTTA 60
 Db 1 ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGGATCCTTATAGTGACACCCCACTTA 60
 QY 61 ATCAGCCTCTACTTCTATAGTGTATTGCGGGCTGCTGGGTGTCATTTCCATTCCTTTC 120
 Db 61 ATCAGCCTCTACTTCTATAGTGTATTGCGGGCTGCTGGGTGTCATTTCCATTCCTTTC 120
 QY 121 CTCCTGGTGAATGAACACCCGGTCAGTGACACCATCGCGGTCAATTAACCTGTTGGTGG 180
 Db 121 CTCCTGGTGAATGAACACCCGGTCAGTGACACCATCGCGGTCAATTAACCTGTTGGTGG 180
 QY 181 GTCACAGAGGTTTCTGCTGACAGGCCATTTGCGCTTGCACCTACCTCATCAAGAGACT 240
 Db 181 GTCACAGAGGTTTCTGCTGACAGGCCATTTGCGCTTGCACCTACCTCATCAAGAGACT 240
 QY 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
 Db 241 TGGATGTTTGGGCTGCCCTTCTGCAAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300
 QY 301 CTCACGTTCTTATCTATGTTGATCCTGGTGACAGATACCTCATCTTCTTCAAGTGC 360
 Db 301 CTCACGTTCTTATCTATGTTGATCCTGGTGACAGATACCTCATCTTCTTCAAGTGC 360
 QY 361 AAAGACAAAGTGGAAATCTACAGAAAACCTGATGCTGCTGCCAGTCTGCCATGTGG 420
 Db 361 AAAGACAAAGTGGAAATCTACAGAAAACCTGATGCTGCTGCCAGTCTGCCATGTGG 420
 QY 421 AGCTGGTGAATGTCATTTGCTGATGCCCTGTTGTCCTCCGGTATGGAATCCATGAGAA 480
 Db 421 AGCTGGTGAATGTCATTTGCTGATGCCCTGTTGTCCTCCGGTATGGAATCCATGAGAA 480
 QY 481 TACAATGAGGAGCAGCTGTTTTAAATTTCAAGAGCTTGTTCACACATATCTGAAAAATC 540
 Db 481 TACAATGAGGAGCAGCTGTTTTAAATTTCAAGAGCTTGTTCACACATATCTGAAAAATC 540
 QY 541 ATCAACTATATGATGATCAATTTTGTATAGCGTTGCTGTGATTTCTGTGTTCTTCCAG 600
 Db 541 ATCAACTATATGATGATCAATTTTGTATAGCGTTGCTGTGATTTCTGTGTTCTTCCAG 600
 QY 601 GTCTTCATCATTTATGTTGATGCTGAGAGCTACCGCACTCTTTACTATCCACAGGAG 660
 Db 601 GTCTTCATCATTTATGTTGATGCTGAGAGCTACCGCACTCTTTACTATCCACAGGAG 660
 QY 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCC 720
 Db 661 TTCTGGGCTCAGCTGAAAAACCTATTTTATAGGGGTCACTCTGTTGTTTCTTCC 720
 QY 721 TACCAGTTCTTTAGGATCTATTAAGTGTGAGCAATCCCAATCCCTGTAAACAGC 780
 Db 721 TACCAGTTCTTTAGGATCTATTAAGTGTGAGCAATCCCAATCCCTGTAAACAGC 780

Db 361 AAAGACAAAGTGAATCTACAGAAAACCTGCATGCTGTGGCTGCCAGTGGCATGTGG 420
 Qy 421 AGCTGGTGAATGTCATTTGTTGTAACCCCTGGTGTCTCCCGTATGGAATCCATGAGAA 480
 Db 421 AGCTGGTGAATGTCATTTGTTGTAACCCCTGGTGTCTCCCGTATGGAATCCATGAGAA 480
 Qy 481 TACAATGAGGACACTGTTTAAATTCACAAGAGCTTGCTTACACATATGTGAAATC 540
 Db 481 TACAATGAGGACACTGTTTAAATTCACAAGAGCTTGCTTACACATATGTGAAATC 540
 Qy 541 ATCAACTATATGATAGTCAATTTTGTCAATGAGCCGTTGCTGTGATCTGTGGTCTTCCAG 600
 Db 541 ATCAACTATATGATAGTCAATTTTGTCAATGAGCCGTTGCTGTGATCTGTGGTCTTCCAG 600
 Qy 601 GTCCTCATCATTTGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACAGAG 660
 Db 601 GTCCTCATCATTTGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACAGAG 660
 Qy 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCATCTTTGTTGTTTCTTCCC 720
 Db 661 TTCTGGGCTCAGCTGAAAACCTATTTTATAGGGGTCATCTTTGTTGTTTCTTCCC 720
 Qy 721 TACAGTCTTTAGGATCTATTACTTTGATGTCAGGCTTCAATGCTGCTGATGTTG 780
 Db 721 TACAGTCTTTAGGATCTATTACTTTGATGTCAGGCTTCAATGCTGCTGATGTTG 780
 Qy 781 AAGGTTGCAATTTATAACGAATCTTCTTGAAGTAAACAGCAATAGCTGCTATGATTG 840
 Db 781 AAGGTTGCAATTTATAACGAATCTTCTTGAAGTAAACAGCAATAGCTGCTATGATTG 840
 Qy 841 CTTCTCTTTGCTTTGGGGGAGCCATTTGTTTGAAGCAAAAGATATGCTTATGGAAT 900
 Db 841 CTTCTCTTTGCTTTGGGGGAGCCATTTGTTTGAAGCAAAAGATATGCTTATGGAAT 900
 Qy 901 TGTGTTTGTGCGGTTAG 918
 Db 901 TGTGTTTGTGCGGTTAG 918

RESULT 4
 ID ABZ59171
 AC ABZ59171;
 DT 28-APR-2003 (first entry)
 DE Human TGR343 protein encoding DNA.
 KW G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;
 KW TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephroretropic;
 KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;
 KW immunosuppressive; antiinflammatory; gene; de.
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT CDS 1..918
 FT /*tag= a
 FT /product= "TGR343"
 XX
 PN WO2003004678-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 01-JUL-2002; 2002WO-US020860.
 XX
 PR 03-JUL-2001; 2001US-0302800P.
 XX
 PA (TULA-) TULARIX INC.
 XX
 PI Tian H, Dai K, Chen J, Zhao J, Cutler G;
 XX

DR WPI: 2003-210368/20.
 DR P-PSDB; ABP71378.
 XX
 FT New G-protein coupled receptor polypeptides designated TGR2, TGR38,
 FT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs
 FT for treating or preventing e.g. asthma, multiple sclerosis, stroke or
 FT nephrolithiasis.
 XX
 XX Claim 7; Page 61; 74pp; English.
 PS
 XX The invention provides new G-protein coupled receptor (GPCR) polypeptides
 CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding
 CC polynucleotides. The polypeptides can be expressed by standard DNA
 CC recombination methodology. The polypeptides are useful for screening or
 CC identifying modulators of GPCR or signal transduction. The modulators of
 CC signal transduction are useful for treating or preventing TGR-associated
 CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The
 CC polypeptides are useful as targets for diagnosing or treating e.g.
 CC epilepsy, stroke, neurodegeneration, hypernatremia, hyperprolactinemia,
 CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,
 CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute
 CC inflammatory dermatoses. The present sequence represents a human TGR343
 CC protein encoding DNA
 XX
 SQ Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
 Query Match 100.0%; Score 918; DB 7; Length 918;
 Best Local Similarity 100.0%; Pred. NO. 0;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGCTGGCCACATACCTCCAGAAATTCCTTTGGGATCCTATAGTGACACCCCACTTA 60
 Db 1 ATGCTGGCCACATACCTCCAGAAATTCCTTTGGGATCCTATAGTGACACCCCACTTA 60
 Qy 61 ATCAGCCTCTACTTCATAGTCTTATTTGGCGGCTGGTGGGTGTCATTTCCATCTTTTC 120
 Db 61 ATCAGCCTCTACTTCATAGTCTTATTTGGCGGCTGGTGGGTGTCATTTCCATCTTTTC 120
 Qy 121 CTCCTGGTGAATGAACACCGGTGACGACCATGACCATGCGGTCAATTAACCTTGTGTG 180
 Db 121 CTCCTGGTGAATGAACACCGGTGACGACCATGACCATGCGGTCAATTAACCTTGTGTG 180
 Qy 181 GTCCACAGCGTTTTTCTGCTGACAGTGCCCAATTTGCGTTGACCTCATCAAGAAGACT 240
 Db 181 GTCCACAGCGTTTTTCTGCTGACAGTGCCCAATTTGCGTTGACCTCATCAAGAAGACT 240
 Qy 241 TGGATGTTGGGCTGCCCTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300
 Db 241 TGGATGTTGGGCTGCCCTCTGCAAAATTTGAGTGCCATGCTGCACATCCACATGTAC 300
 Qy 301 CTCAGCTTCTTATTTCTATGTTGATCCTGCTCAACAGATACCTCATCTTCTTCAAGTGC 360
 Db 301 CTCAGCTTCTTATTTCTATGTTGATCCTGCTCAACAGATACCTCATCTTCTTCAAGTGC 360
 Qy 361 AAAGACAAAGTGAATCTACAGAAAACCTGCATGCTGTGGCTGCCAGTGGCATGTGG 420
 Db 361 AAAGACAAAGTGAATCTACAGAAAACCTGCATGCTGTGGCTGCCAGTGGCATGTGG 420
 Qy 421 AGCTGGTGAATGTCATTTGTTGTAACCCCTGGTGTCTCCCGTATGGAATCCATGAGAA 480
 Db 421 AGCTGGTGAATGTCATTTGTTGTAACCCCTGGTGTCTCCCGTATGGAATCCATGAGAA 480
 Qy 481 TACAATGAGGACACTGTTTAAATTCACAAGAGCTTGCTTACACATATGTGAAATC 540
 Db 481 TACAATGAGGACACTGTTTAAATTCACAAGAGCTTGCTTACACATATGTGAAATC 540
 Qy 541 ATCAACTATATGATAGTCAATTTTGTCAATGAGCCGTTGCTGTGATCTGTGGTCTTCCAG 600
 Db 541 ATCAACTATATGATAGTCAATTTTGTCAATGAGCCGTTGCTGTGATCTGTGGTCTTCCAG 600
 Qy 601 GTCCTCATCATTTGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACAGAG 660
 Db 601 GTCCTCATCATTTGTTGATGTCAGAGCTACGCCACTCTTTACTATCCACAGAG 660

Dd	1	ATGCTGGCCACAATACCTCCAGGAATTCCTCTTGGCATCCTATAGTGACACCCCACTTA	60
Qy	61	ATCAGCCTCTACTTTCATAGTGCTTATTGGCGGGCTGGTGGGTGTCATTTTCCATTTCTTTTC	120
Dd	61	ATCAGCCTCTACTTTCATAGTGCTTATTGGCGGGCTGGTGGGTGTCATTTTCCATTTCTTTTC	120
Qy	121	CTCCTGGTGAAATGAACACCGGTFCAGTGACACCAATGGGGTCATTAACCTGGTGGTG	180
Dd	121	CTCCTGGTGAAATGAACACCGGTFCAGTGACACCAATGGGGTCATTAACCTGGTGGTG	180
Qy	181	GTCCACAGCGTTTTTCTGTGACAGTGCCATTTGGTGTGACCTACCTCATCAAGAAGACT	240
Dd	181	GTCCACAGCGTTTTTCTGTGACAGTGCCATTTGGTGTGACCTACCTCATCAAGAAGACT	240
Qy	241	TGGAATGTTGGGCTGCCCTTCTGCAAAATTTGTGATGGCAATGTCGACATCCACATGTAC	300
Dd	241	TGGAATGTTGGGCTGCCCTTCTGCAAAATTTGTGATGGCAATGTCGACATCCACATGTAC	300
Qy	301	CTCACGTTCCCTATTCTATGTGTGATCCTGTGTCACCCAGATACCTCATCTTTTCAAGTGC	360
Dd	301	CTCACGTTCCCTATTCTATGTGTGATCCTGTGTCACCCAGATACCTCATCTTTTCAAGTGC	360
Qy	361	AAAGCAAAAGTGGAAATCTACAGAAAACTGCATGCTGTGGCTGGCAGTGCCTGGCATGTGG	420
Dd	361	AAAGCAAAAGTGGAAATCTACAGAAAACTGCATGCTGTGGCTGGCAGTGCCTGGCATGTGG	420
Qy	421	AGCTGGTGATTTGTCATTGTGTGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA	480
Dd	421	AGCTGGTGATTTGTCATTGTGTGTACCCCTGGTGTCTCCCGGTATGGAATCCATGAGGAA	480
Qy	481	TACAAATGAGGAGCATGTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAAATC	540
Dd	481	TACAAATGAGGAGCATGTGTTTAAATTTCAAAAGAGCTTGCTTACACATATGTGAAAAATC	540
Qy	541	ATCAACTATATGATAGTCATTTTGTGTCATAGCCGTGCTGTGATCTGTGTGCTTCCAG	600
Dd	541	ATCAACTATATGATAGTCATTTTGTGTCATAGCCGTGCTGTGATCTGTGTGCTTCCAG	600
Qy	601	GTCTTCATCATTTATGTGATGTGCAGAAAGTACGCCACTCTTTTACTATCCCAACGAGG	660
Dd	601	GTCTTCATCATTTATGTGATGTGCAGAAAGTACGCCACTCTTTTACTATCCCAACGAGG	660
Qy	661	TTCTGGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTGCATCCTGTGTGTTTCTTCC	720
Dd	661	TTCTGGGCTCAGCTGAAAAACCTATTTTTTATAGGGGTGCATCCTGTGTGTTTCTTCC	720
Qy	721	TACCACTTCTTTAGATCTATTACTTTGAATGTTGTGACGCAATCCCAATGCTGTAACAGC	780
Dd	721	TACCACTTCTTTAGATCTATTACTTTGAATGTTGTGACGCAATCCCAATGCTGTAACAGC	780
Qy	781	AAGTTGCAATTTTAAAGCAATCTTCTTGTAGTGTAAACGCAATAGCTGCTATGATTTTG	840
Dd	781	AAGTTGCAATTTTAAAGCAATCTTCTTGTAGTGTAAACGCAATAGCTGCTATGATTTTG	840
Qy	841	CTTCTCTTTGCTTTTGGGGAGCCATTGGTTTAAAGCAAAAGATAAATGGCTTATGGAAT	900
Dd	841	CTTCTCTTTGCTTTTGGGGAGCCATTGGTTTAAAGCAAAAGATAAATGGCTTATGGAAT	900
Qy	901	TGTTGTTTCTGCCGTTAG	918
Dd	901	TGTTGTTTCTGCCGTTAG	918

RESULT 3	
ABT04867	
ID	ABT04867 standard; cDNA; 918 BP.
XX	
XX	
AC	ABT04867;
XX	
DT	11-OCT-2002 (first entry)
XX	
DE	Human G protein coupled receptor hrUP29 coding sequence.
XX	
XX	

KW	Human; G-protein coupled receptor GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
KW	hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.
XX	
XX	Homo sapiens.
XX	WO200242461-A2.
XX	
XX	30-MAY-2002.
PD	
XX	
XX	26-NOV-2001; 2001WO-US044386.
XX	
XX	27-NOV-2000; 2000US-0253404P.
PR	12-DEC-2000; 2000US-0250366P.
PR	20-FEB-2001; 2001US-0270266P.
PR	20-FEB-2001; 2001US-0270286P.
PR	06-APR-2001; 2001US-0282032P.
PR	06-APR-2001; 2001US-0282356P.
PR	06-APR-2001; 2001US-0282358P.
PR	06-APR-2001; 2001US-0282365P.
PR	14-MAY-2001; 2001US-0290917P.
PR	31-JUL-2001; 2001US-0309208P.
XX	
XX	(AREN-) ARENA PHARM INC.
PA	
XX	Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
XX	WPI; 2002-566565/60.
XX	P-PSDB; ABJ04069.
DR	
XX	Novel endogenous and non-endogenous versions of G protein-coupled
PT	receptor useful for identification of candidate compounds as receptor
PT	agonists or antagonists for use as therapeutic agents.
XX	
XX	Claim 7; Page 56-57; 84pp; English.
PS	
XX	
XX	The present invention provides the protein and coding sequences of
CC	several human G-protein coupled receptors (GPCRs). These can be used in
CC	the identification of candidate compounds as receptor agonists or inverse
CC	agonists having applicability as therapeutic agents. The present sequence
CC	is a GPCR coding sequence of the invention
XX	
XX	Sequence 918 BP; 208 A; 207 C; 201 G; 302 T; 0 U; 0 Other;
SQ	
Query Match 100.0%; Score 918; DB 6; Length 918;	
Best Local Similarity 100.0%; Pred. No. 0;	
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 ATCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCACTTA 60
Db	1 ATCCCTGGCCACAAATACCTCCAGGAATTCCTCTTGGATCCTATAGTGACACCCACTTA 60
Qy	61 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGCTGGTGGGTGTCATTTCCATTCCTTTTC 120
Db	61 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGCTGGTGGGTGTCATTTCCATTCCTTTTC 120
Qy	121 CTCTGGTGAATGACACCCGGTCAGTGACACCACTGGCGGTGTCATTAATGCTGGTGGTG 180
Db	121 CTCTGGTGAATGACACCCGGTCAGTGACACCACTGGCGGTGTCATTAATGCTGGTGGTG 180
Qy	181 GTCACAGCGCTTTTCTGCTGACAGTGCCATTTCGGCTTGACCTACCTCATCAAGAAGACT 240
Db	181 GTCACAGCGCTTTTCTGCTGACAGTGCCATTTCGGCTTGACCTACCTCATCAAGAAGACT 240
Qy	241 TGGATGTTGGGCTGGCTTCTGCAAAATTTGTGAGTGCCATGTGCATCCACATGTCATC 300
Db	241 TGGATGTTGGGCTGGCTTCTGCAAAATTTGTGAGTGCCATGTGCATCCACATGTCATC 300
Qy	301 CTCAGGTTCCATTTCTATGTGGTGATCCCTGGTCACAGATACCTCATCTTCTTCAAGTGC 360
Db	301 CTCAGGTTCCATTTCTATGTGGTGATCCCTGGTCACAGATACCTCATCTTCTTCAAGTGC 360
Qy	361 AAAGACAAAGTGAATTTCTACAAAACTGCAATGCTGTGGCTGCCAGTGTGGCATGTGG 420

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 15:49:39 ; Search time 452 Seconds
(without alignments)
8627.978 Million cell updates/sec

Title: US-10-055-106C-1

Perfect score: 918

Sequence: 1 atgctggccacaatacctc.....attgtgtttgtgcgcttag 918

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 2124099041 residues

Word size : 12

Total number of hits satisfying chosen parameters: 258324

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	6	AAL44713 Human tes
2	918	100.0	918	6	ABA00160 PFT-021 c
3	918	100.0	918	6	ABT04867 Human G p
4	918	100.0	918	7	ABZ59171 Human TGR
5	918	100.0	1040	8	AAL57070 Human G-p
6	918	100.0	1336	6	AAT88583 Human GCR
7	918	100.0	1340	6	AAT88584 Human GCR
8	918	100.0	1460	6	AAT88585 Human GCR
9	918	100.0	2525	6	AAT88585 Human GCR
10	918	100.0	2525	6	ABZ59182 Human TGR
11	918	100.0	113306	9	ABT04879 Human G p
12	887	96.6	1499	6	ABT04879 Human G p
13	867	94.4	1051	6	ABK87351 Human GCR
14	867	94.4	1684	6	AAL53413 1684 nt c
15	864	94.1	939	6	AAL53414 939 nt co
16	690	75.2	972	9	ADC12789 Human GPC
17	306	33.3	447	4	AAT88585 Human GCR
18	306	33.3	447	6	ABZ59182 Human TGR
19	162	17.6	479	4	AAK56763 Human imm
20	39	4.2	29	6	ABK87351 Human GCR
21	29	3.2	29	6	ABT04881 Human G p
22	28	3.1	28	6	ABT04880 Human G p
23	27	2.9	810	9	ADB78584 Mouse G-p

24	26	2.8	26	6	AAL44718	Testis or
25	26	2.8	26	6	ABT04906	Human G p
C 26	25	2.7	25	8	AAL57075	TagMan pr
C 27	24	2.6	24	4	AAH51055	Oligonucle
C 28	24	2.6	24	4	AAH51084	Human nGP
C 29	24	2.6	24	4	AAL44715	Testis or
C 30	24	2.6	24	6	ABZ70288	nGPCR-x r
C 31	24	2.6	24	6	ABZ70317	PCR prime
C 32	24	2.6	24	8	AAL57073	TagMan pr
33	24	2.6	26	6	ABT04878	Human G p
C 34	24	2.6	52	4	AAH51085	Human nGP
C 35	24	2.6	52	4	AAH51056	Oligonucle
C 36	24	2.6	52	6	ABZ70318	PCR prime
C 37	24	2.6	52	6	ABZ70289	nGPCR-x r
38	23	2.5	23	4	AAH51057	Oligonucle
39	23	2.5	23	4	AAH51086	Human nGP
40	23	2.5	23	6	ABZ70319	PCR prime
41	23	2.5	23	6	ABZ70290	nGPCR-x r
C 42	23	2.5	23	7	ABZ59182	Human TGR
C 43	23	2.5	31	6	ABT04879	Human G p
C 44	23	2.5	31	6	ABT04907	Human G p
C 45	23	2.5	34	4	AAH51033	Human nGP

ALIGNMENTS

RESULT 1					
AAL44713					
ID	AAL44713 standard; DNA; 918 BP.				
XX					
AC	AAL44713;				
XX					
DT	03-MAY-2002 (first entry)				
XX					
DE	Human testis originated G-protein coupled receptor TGR10 coding sequence.				
XX					
KW	Human; testis-originated G-protein coupled receptor; TGR10; inflammatory;				
KW	cytostatic; immunomodulator; cardiac; neuroprotective; gene therapy;				
KW	inflammation; nervous system disease; circulatory system disease; cancer;				
KW	metabolic disease; immunological disease; gastrointestinal disease; gene;				
XX	ds.				
XX	Homo sapiens.				
OS					
PH	Key Location/Qualifiers				
FT	1..918				
FT	/*tag= a				
FT	/product= "TGR10"				
XX					
XX	WO200196567-A1.				
XX					
PD	20-DEC-2001.				
XX					
PP	14-JUN-2001; 2001WO-JP005061.				
XX					
PR	15-JUN-2000; 2000JP-00184596.				
PR	19-JUL-2000; 2000JP-00223887.				
XX					
PA	(TAKE) TAKEDA CHEM IND LTD.				
XX					
PI	Moriya T, Ito T, Shintani Y, Miyajima N;				
XX					
DR	WPI; 2002-098071/13.				
XX					
XX	P-PSDB; AAM48989.				
XX					
PT	Human testis-originated G protein-coupled receptor protein TGR10 and				
PT	encoded DNA, useful for gene diagnosis and developing drugs to treat e.g.				
PT	diseases of central nervous system, inflammations and diseases of				
PT	circulatory system.				
XX					
PS	Claim 5; Page 99; 110pp; Japanese.				
XX					

```
Query Match      1.9%; Score 17; DB 4; Length 801;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 TGTGTTTAATTCACAA 512
DB 18 TGTGTTTAATTCACAA 2

RESULT 14
US-09-489-039A-1185/c
; Sequence 1185, Application US/09489039A
; Patent No. 6810936
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1185
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1185

Query Match      1.9%; Score 17; DB 4; Length 978;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 ACCACCATGGGGTCAT 167
DB 260 ACCACCATGGGGTCAT 244

RESULT 15
US-09-833-381-461
; Sequence 461, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 461
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-461

Query Match      1.9%; Score 17; DB 4; Length 1057;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 GTTGATGTCGAGAGC 631
DB 704 GTTGATGTCGAGAGC 720

Search completed: April 25, 2004, 19:58:29
Job time : 95 secs
```

```
|||||
Db 3981 TATTGCGGCGTGTGGG 3998

RESULT 9
US-09-734-673-3/c
; Sequence 3, Application US/09734673
; Patent No. 6410294
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001020
; CURRENT APPLICATION NUMBER: US/09/734,673
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 38564
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..-(38564)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-673-3

Query Match 2.0%; Score 18; DB 4; Length 38564;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 306 GTTCCTATTCTATGTGGT 323
Db 34622 GTTCCTATTCTATGTGGT 34605

RESULT 10
US-09-313-294A-940
; Sequence 940, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 940
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700550095H1
US-09-313-294A-940

Query Match 1.9%; Score 17; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 581 TGATTCTGTGTCCTTC 597
Db 39 TGATTCTGTGTCCTTC 55

RESULT 11
US-09-833-381-1029/c
; Sequence 1029, Application US/09833381
; Patent No. 6672186

; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs.
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1029
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(472)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1029

Query Match 1.9%; Score 17; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 TGAGTGCCATGCTGCAC 288
Db 220 TGAGTGCCATGCTGCAC 204

RESULT 12
US-09-540-236-1026
; Sequence 1026, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1026
; LENGTH: 648
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-1026

Query Match 1.9%; Score 17; DB 4; Length 648;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 402 TGCCAGTGTGTCATGT 418
Db 279 TGCCAGTGTGTCATGT 295

RESULT 13
US-09-540-236-1020/c
; Sequence 1020, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1020
; LENGTH: 801
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-1020
```

APPLICATION NUMBER: 07/635,475
FILING DATE: 28-Dec-1990
APPLICATION NUMBER: 07/377,238
FILING DATE: 06-Jul-1984
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: TRV 2 005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Nucleotide-genomic DNA
HYPOTHETICAL: Irrelevant
ANTI-SENSE: Irrelevant
FRAGMENT TYPE: Endonuclease restriction
FRAGMENT TYPE: fragment
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: Irrelevant
INDIVIDUAL ISOLATE: Irrelevant
DEVELOPMENTAL STAGE: Irrelevant
HAPLOTYPE: Irrelevant
TISSUE TYPE: Lung
CELL TYPE: Irrelevant
CELL LINE: Irrelevant
ORGANELLE: Irrelevant
IMMEDIATE SOURCE:
LIBRARY: Human genomic in lambda
LIBRARY: FIX vector
CLONE: F8
POSITION IN GENOME:
CHROMOSOME/SEGMENT: X
MAP POSITION: q22
UNITS: Irrelevant
FEATURE:
NAME/KEY: COL4A5 collagen gene
LOCATION: Exon 16 region from 3',
LOCATION: end of gene
IDENTIFICATION METHOD: DNA sequencing
OTHER INFORMATION: The sequence contains 100
OTHER INFORMATION: nucleotides from intron 16 (lower case letters),
OTHER INFORMATION: nucleotides exon 16 (capital letters) and 24
OTHER INFORMATION: nucleotides of intron 15 (lower case letters).
US-08-692-989-16
Query Match 2.0%; Score 18; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 589 TTGGTCTTCAGGCTTC 606
Db 212 TTGGTCTTCAGGCTTC 229
RESULT 6
US-09-328-352-3416
Sequence 3416, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 3416
LENGTH: 684
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-3416
Query Match 2.0%; Score 18; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 611 TTATGTTGATGGTGCGA 628
Db 252 TTATGTTGATGGTGCGA 269
RESULT 7
US-09-252-991A-10198/c
Sequence 10198, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10198
LENGTH: 1311
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10198
Query Match 2.0%; Score 18; DB 4; Length 1311;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 84 TATTGGGGGCTGGTGGG 101
Db 325 TATTGGGGGCTGGTGGG 308
RESULT 8
US-09-252-991A-9867
Sequence 9867, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9867
LENGTH: 4248
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9867
Query Match 2.0%; Score 18; DB 4; Length 4248;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 84 TATTGGGGGCTGGTGGG 101

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ATCAAGAAGACTTGGATGT 247
 DB 158 ATCAAGAAGACTTGGATGT 176

RESULT 2
 US-09-171-410-2
 ; Sequence 2, Application US/09171410
 ; Patent No. 6194187
 ; GENERAL INFORMATION:
 ; APPLICANT: MIYAZONO, Kohel
 ; APPLICANT: ICHIGO, Hidenori
 ; TITLE OF INVENTION: APOPTOSIS-INDUCING PROTEIN AND GENE ENCODING THE SAME
 ; FILE REFERENCE: 04941/0117
 ; CURRENT APPLICATION NUMBER: US/09/171,410
 ; CURRENT FILING DATE: 1998-10-19
 ; EARLIER APPLICATION NUMBER: PCT/JP97/01348
 ; EARLIER FILING DATE: 1997-04-18
 ; EARLIER APPLICATION NUMBER: JP 241063/1996
 ; EARLIER FILING DATE: 1996-08-23
 ; EARLIER APPLICATION NUMBER: JP 122320/1996
 ; EARLIER FILING DATE: 1996-04-19
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 4533
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (288)..(4392)
 US-09-171-410-2

Query Match 2.1%; Score 19; DB 3; Length 4533;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ATCAAGAAGACTTGGATGT 247
 DB 3833 ATCAAGAAGACTTGGATGT 3851

RESULT 3
 US-09-359-757-1
 ; Sequence 1, Application US/09359757
 ; Patent No. 6080546
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: William Gaarde
 ; APPLICANT: Lex M. Coward
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF MEK5 EXPRESSION
 ; FILE REFERENCE: RFS-0078
 ; CURRENT APPLICATION NUMBER: US/09/359,757
 ; CURRENT FILING DATE: 1999-07-23
 ; NUMBER OF SEQ ID NOS: 47
 ; SEQ ID NO 1
 ; LENGTH: 5236
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (361)..(4485)
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: 4687
 ; OTHER INFORMATION: unknown
 US-09-359-757-1

Query Match 2.1%; Score 19; DB 3; Length 5236;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ATCAAGAAGACTTGGATGT 247
 DB 3923 ATCAAGAAGACTTGGATGT 3941

RESULT 4
 US-09-252-991A-10058/c
 ; Sequence 10058, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 10058
 ; LENGTH: 258
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-10058

Query Match 2.0%; Score 18; DB 4; Length 258;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 TATTGGCGGCTGGTGGG 101
 DB 255 TATTGGCGGCTGGTGGG 238

RESULT 5
 US-08-692-989-16
 ; Sequence 16, Application US/08692989
 ; Patent No. 6576418
 ; GENERAL INFORMATION:
 ; APPLICANT: Irygvason, Karl
 ; APPLICANT: Hostikka, Sirkka L.
 ; APPLICANT: Zhou, Jing
 ; TITLE OF INVENTION: Method for Determining the
 ; TITLE OF INVENTION: Nucleotide Sequence of the Gene
 ; Patent No. 6576418
 ; TITLE OF INVENTION: for the '5(IV) Chain of Human
 ; TITLE OF INVENTION: Type IV Collagen
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fay, Sharpe, Beall, Fagan,
 ; ADDRESSEE: Minnich & McKee
 ; STREET: 1100 Superior Avenue
 ; STREET: Suite 700
 ; CITY: Cleveland
 ; STATE: Ohio
 ; COUNTRY: U.S.A.
 ; ZIP: 44114-2518
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch,
 ; MEDIUM TYPE: 720 Kb storable
 ; COMPUTER: IBM PS/2, Model 35 SX
 ; OPERATING SYSTEM: DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/692,989
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/346,336
 ; FILING DATE: 29-NOV-1994

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 17:46:14 ; Search time 91 Seconds
(without alignments)
5598.296 Million cell updates/sec

Title: US-10-055-106C-1
Perfect score: 918
Sequence: 1 atgctggccacaatactc.....attgtgtttgtgcgcttag 918

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 12

Total number of hits satisfying chosen parameters: 30028

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	19	2.1	263	4	US-09-016-434-168
2	19	2.1	433	3	US-09-171-410-2
3	19	2.1	5236	3	US-09-359-757-1
4	18	2.0	258	4	US-09-252-991A-10058
5	18	2.0	264	4	US-08-692-989-16
6	18	2.0	684	4	US-09-328-352-3416
7	18	2.0	1311	4	US-09-252-991A-10198
8	18	2.0	4248	4	US-09-252-991A-9867
9	18	2.0	38564	4	US-09-734-673-3
10	17	1.9	258	4	US-09-313-294A-940
11	17	1.9	472	4	US-09-833-381-1029
12	17	1.9	648	4	US-09-540-236-1026
13	17	1.9	801	4	US-09-540-236-1020
14	17	1.9	978	4	US-09-489-039A-1185
15	17	1.9	1057	4	US-09-833-381-461
16	17	1.9	1322	4	US-09-976-594-310
17	17	1.9	1761	3	US-09-033-055A-3
18	17	1.9	2098	2	US-08-937-931-5
19	17	1.9	2098	3	US-09-285-502-5
20	17	1.9	2098	4	US-09-709-126-5
21	17	1.9	2098	4	US-09-871-385A-5
22	17	1.9	2100	1	US-08-332-576-1
23	17	1.9	2100	5	PCT-US95-13672-1
24	17	1.9	2998	4	US-09-081-385-4
25	17	1.9	2998	4	US-09-081-385-149
26	17	1.9	3014	2	US-08-808-982-1
27	17	1.9	3014	3	US-09-306-902A-1

C	28	17	1.9	5280	4	US-08-956-171E-544
	29	17	1.9	269223	4	US-09-596-002-41
C	30	17	1.9	269223	4	US-09-596-002-41
C	31	17	1.9	640681	4	US-09-790-988-1
C	32	17	1.9	786431	4	US-09-751-389-3
C	33	17	1.9	1664976	4	US-08-916-421B-1
C	34	17	1.9	1830121	4	US-09-557-884-1
	35	17	1.9	1830121	4	US-09-643-990A-1
C	36	16	1.7	207	4	US-09-328-352-2491
	37	16	1.7	288	4	US-09-313-294A-4045
	38	16	1.7	366	4	US-09-397-787-268
C	39	16	1.7	436	4	US-09-592-126-133
C	40	16	1.7	503	1	US-08-592-126-133
C	41	16	1.7	503	4	US-09-168-595-133
C	42	16	1.7	513	1	US-08-462-894-15
C	43	16	1.7	513	1	US-08-206-185-15
C	44	16	1.7	516	1	US-08-462-894-14
C	45	16	1.7	516	1	US-08-462-894-16

ALIGNMENTS

RESULT 1
US-09-016-434-168
; Sequence 168, Application US/09016434
; Patent No. 650938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA: US/09/016,434
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT12
; CLONE: 1413041
; US-09-016-434-168

Query Match 2.1%; Score 19; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 6.8;

Percent Similarity:	46.57%	Conservative:	54
Best Local Similarity:	27.08%	Mismatches:	128
Query Match:	13.63%	Indels:	20
DB:	2	Gaps:	12
US-10-055-106C-2 (1-305) x US-08-467-948A-7 (1-1301)			
Qy	23	LeuTyrPheIleValLeuIleGlyGlyLeuVal---GlyValIleSerIleLeuPheLeu	41
Db	227	ATGTTACAGCATGGTGGTGGTAAATCAATTTGTTGGCATATACATTTTC	286
Qy	42	LeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal	61
Db	287	ATCTGCGTCTCTAAAGTCCGAATGAACTACAACTTACATGATTAACTTGGCAATGCA	346
Qy	62	HisSerValPheLeuLeuValProPheArgLeuThrTyrLeuIleLysLysThrTyr	81
Db	347	GACTTGGTTTTGTTTTACTTTACCTTCAGGATTTTACTTCACACACGGAATGG	406
Qy	82	MetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyrLeu	101
Db	407	CCATTGGAGATTACTTTGTAGATTCTGTGATGCTGTTTTATACCAACATGTACGGA	466
Qy	102	ThrPheLeuPheTyrValValIleLeuValThrArgTyrLeu---IlePhePheLysCys	120
Db	467	AGCATTCGTCTTAACCTGRTTAGTGTAGATCGATTTCTGGCAATTGCTACCCATTT	526
Qy	121	LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaLaserAlaGlyMetTyr	140
Db	527	AAGTCAAAAGACT---CTAAGAACCAAGAAATGCAAAAGATTGTTGCACCTGGCGTGTGG	583
Qy	141	ThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHisGluGlu	160
Db	584	TTAACCTGTGATCGAGGAGTGACCCCGCTTTTGTTCAG---TCTACCCACTCTCAG	640
Qy	161	TyrAsn-----GluGluHisCysPheLysPheHisLysGluLeuAlaTyr---ThrTyr	177
Db	641	GGTAACAATGCCTCAGAAGCCTGCTTTGAAAAATTTCCAGAGCCACATGGAACATAT	700
Qy	178	ValLysIleIleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeu---	196
Db	701	CTCTCA-----AGGATTGTAATTTTCATCGAAATAGTGGGATTTTATTTCCT	748
Qy	197	LeuValPheGlnValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeu---	215
Db	749	CTAATTTTAATGTAATCTTCTAGTATGGTGTAAAACTTTAACCAACCTGTTACA	808
Qy	216	LeuSerHisGlnGluPhe---TrpAlaGlnLysAsnLeuPhePheIleGlyValIle	234
Db	809	TAAAGTAGAAGCAAAATAACAAACTAAGGTTTTAAAAATGATTTTGTACATTGATC	868
Qy	235	Leu-----ValCysPheLeuProTyrGlnPhePheArgIleTyrTyrLeuAsnValVal	252
Db	869	ATATTCTGTTTCTGTTTGTTCCTTCAATATCAATCTTATTTATATTCTCTGTGAGA	928
Qy	253	ThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsnGluIlePheLeuSerVal	272
Db	929	ACACAAACATTGTTAATTTGCTACGTAGTGGCAGCAGTAAGGACAAATGTACCCAATCACT	988
Qy	273	ThrAlaIleSer-----CysTyrAspLeuLeuLeuPheValPhe	285
Db	989	CTCTGATTGCTGTTTCCAACTGTTGTTTGGACCTATAGTTTACTACTTT	1039

Search completed: April 25, 2004, 22:26:10
Job time : 94 secs

QY	216	LeuSerHisGlnGluPhe---TrrAlaGlnLeuLysAsnLeuPheHeilegLyValle	234
Db	694	TTrAGTAGACAAATAAACAACCTAAGTTTAAAAATGATTITGTACATTTCATC	753
QY	235	Leu-----ValCysPheLeuProTyrGlnPhePhearglleTyrTyrrLeuasnVal	252
Db	754	ATATTCTGTTCTGTTTGTCTTCAATATCAATCTTATTTATATTTCTTGGAAGA	813
QY	253	ThrHisSerAsnAlaCysAsnSerLysValalaphetyrAsnGluillePheLeuSerVal	272
Db	814	ACACAACATTGGTTTAATGCTCAGTAGTGGCAGCAGTAAAGCAATGTACCACACT	873
QY	273	ThralalleSer-----CystyrAspLeuLeuLeuPheValPhe	285
Db	874	CTCTGATTGCTGTTTCCAACTGTTGTTGACCCCTATAGTTTACTACTTT	924
RESULT 15			
US-08-467-948A-7			
; Sequence 7, Application US/08467948A			
; Patent No. 5998184			
; GENERAL INFORMATION:			
; APPLICANT: LI, YI			
; APPLICANT: CAO, JIAN			
; APPLICANT: NI, JIAN			
; APPLICANT: GENTZ, REINER			
; APPLICANT: BULT, CAROL J.			
; APPLICANT: SUTTON III, GRANGER G.			
; APPLICANT: ROSEN, CRAIG A.			
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein			
; NUMBER OF SEQUENCES: 30			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.			
; STREET: 1100 NEW YORK AVE., NW, SUITE 600			
; CITY: WASHINGTON			
; STATE: DC			
; COUNTRY: USA			
; ZIP: 20005			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: FLOPPY DISK			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/467,948A			
; FILING DATE: 06-JUN-1995			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: PCT/US95/04079			
; FILING DATE: 30-MAR-1995			
; ATTORNEY/AGENT INFORMATION:			
; NAME: STEFFE, ERIC K.			
; REGISTRATION NUMBER: 36,688			
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 202-371-2600			
; TELEFAX: 202-371-2540			
; INFORMATION FOR SEQ ID NO: 7:			
; LENGTH: 1301 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: both			
; TOPOLOGY: both			
; MOLECULE TYPE: cDNA			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 161..1192			
US-08-467-948A-7			
Alignment Scores:			
Pred. No.:	4,766-13	Length:	1301
Score:	217.00	Matches:	75
US-10-055-106C-2 (1-305) x US-09-016-434-750 (1-1140)			
QY	23	LeutyrrPheilleValleuleglycylleuVal---GlyvalleiserrilleuPheleu	41
Db	112	ATGTTCCAGCATGCTGTTGCTGGGTAAATACCAATGCTGTGCATATCAATTTTC	171
QY	42	LeuVallysMetAsnThrArgSerValThrMetAlaValleAsnLeuValVal	61
Db	172	ATCTCGCTCCCAAGTCGGAATCAAACCTAACCTACATGATTAACTTGGCAATGCA	231
QY	62	HisservAlpheLeuThrValProPheargLeuthrTyrrLeulleLysLysThrTip	81
Db	232	GACTTGTCTTTGTTTACTTACCTTCAGGATTTTTTACTTCAACAACAGGAATGG	291
QY	82	MetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisielleHismetTyrrLeu	101
Db	292	CCATTGGAGATTACTTTGTAAGATTCTGTGATGCTGTTTATACCAACATGACGGA	351
QY	102	ThrPheLeuPheTyrrValilleuValThrArgTyrrLeu---llePhePheLysCys	120
Db	352	AGCATCTGTTCTTAACCTGATTAGTGTAGATGATTTCTGGCAATTTGCTACCCATTT	411
QY	121	LysAspLysValgluPheTyrrArgLysLeuHisiAlaValalaaserAlaglymetTip	140
Db	412	RAGTCAAGACT--CTRAAGAACAAAAGAAATGCAAGATTGTTGCACTGGCGGTGG	468
QY	141	ThrLeuValilleValleValProLeuValValSerArgTyrrGlylleHisiGluGlu	160
Db	469	TTAACGTGTGATCGGAGGAAGTGCACCCGCCGTTTTTGTTCAG---TCTACCCATCTCAG	525
QY	161	TyrAsn-----GluGluHisiCysPheLysPheHisiLysGluLeuAlaTyrr---ThrTyrr	177
Db	526	GGTAAACATGCCTCAGAGCCCTGCTTTGAAATTTTCCAGAGCCACATGGAACACATAT	585
QY	178	VallysillelleAsnTyrrMetilleValillePheValilleAlaValAlaValleLeu---	196
Db	586	CTCTCA-----AGGATTGTAATTTTTCAGAAATAGTGGGATTTTTTATTCTCT	633
QY	197	LeuValPheGlnValPheilleMetLeuMetValGlnLysLeuArgHisiSerLeu---	215
Db	634	CTAATTAAAGTAACTGTTCTAGTAGTGGGTAAATAAATTTTAAACCAACCTGTTACA	693

```
RESULT 13
US-09-016-434-1302
; Sequence 1302, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1302:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G307433
; US-09-016-434-1302

Alignment Scores:
Pred. No.: 5,08e-13 Length: 1634
Score: 218.00 Matches: 72
Percent Similarity: 45.89% Conservative: 73
Best Local Similarity: 22.78% Mismatches: 121
Query Match: 13.69% Indels: 50
DB: 4 Gaps: 14

US-10-055-106C-2 (1-305) x US-09-016-434-1302 (1-1634)

Qy 2 ProglyHisAsnThrSerArgAsnSerSer---CysAspProIleValThrProHisLeu 20
Db 220 CCAGGGCGAATCGTCCAGACGGACCTTGAGCGAGGCGCCAGCGCGCATCTG 279
Qy 21 IleSer---LeuTyPheIleValLeuIleGlyLeuValgly-----ValIle 36
Db 280 ATCTCTTCTACTCTCGTGGTGTGCTGGTGGGCTGTGGGAACCTCTAGTGCATC 339
Qy 37 SerIleLeuPheLeuValValMetAsnThrArgSerValThrMetAlaValIle 56
Db 340 TAGTGATCTCGCTATGCCAGATGAAGACG-----CCACCAACATCTACATCCTA 393
Qy 57 AsnLeuValValHisSerValPheLeuThrValProPheArgLeuThrTyLeu 76
Db 394 AATCTGCCCATGTGTGATGAGCTGCTCATGTGTCAGCGTCCCTTCTAGTCACTCCACG 453

Qy 77 IleLysLysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
Db 454 TTGTTGGCCACTGGCCCTTGGTGGCTGCTGGCGCTGCTGGCGCTGCTGGCGCG 513
Qy 97 IleHisMetTyLeuThrPheLeuPheTyValValIleLeuValThrArgTyLeuIle 116
Db 514 GTCAACATGTTTACCAGCATCTACTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 573
Qy 117 PhePheLysCysLysAspLysValGluPheTyArgLysLeuHisAlaValAlaLaser 136
Db 574 GTGGTGCATCCCATCAAGCGCGCCGCTACCGCGCCGCGCCGCGCGCGCGCGCTAA 633
Qy 137 AlaGlyMetTrpThrLeuValIleValIleValValProLeuValVal---SerArgTy 155
Db 634 CTGGGGGTGGTGGTGTATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 693
Qy 156 GlyIleHisGluGluTyAsnGluHisCysPheLysPheHisLysGluLeuAlaTy 175
Db 694 GCGGCCAACAGCGAC---GGCAGCGTGGCTTGCACATGCTCATGCCAGAGCGCGCTCA 750
Qy 176 ThrTy---ValLysIleIleAsnTyMetIleValIle---PheValIleAlaValAla 193
Db 751 CGTGGCTGGTGGCTTCTGTTGTACACATTTCTCATGGGCTTCTGCTGCGCCGTGGG 810
Qy 194 ValIleLeuValPheGlnValPheIleIleMetLeuMetValGlnLysLeuArgHis 213
Db 811 GCTATCTGCTGTGTAC---GTCTCATCTGCTGATGCTGCTGCTGCTGCTGCTGCTG 852
Qy 214 SerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsn----- 227
Db 853 ---ATGGTGGCTCAAGCGCGCTGGCAGCGCGCAAGCGCTCGGAGCGCAAGATCACC 909
Qy 228 -----LeuPhePheIleGlyValIleLeuValCysPheLeuProTyGlnPhePhe 244
Db 910 TTAATGGTGTATGATGGTGTGATGTTGTGTTGTCATCTGCTGATGCTGCTGCTGCT 963
Qy 245 ArgIleTyTyLeuAsnVal----- 251
Db 964 GTGGTGCAGCTGTTTAACTGTTTGTGTCAGCAGGAGCGCGCGCGCGCGCGCTGCTG 1023
Qy 252 -----ValThrHisSerAsnAlaCysAsnSerLysValAlaPhe----- 264
Db 1024 GTCATCTCGGCTATGCCAACAGCTGCGCCACCCCATCTCTATGGGTTTCTCTCAGAC 1083
Qy 265 ---TyAsnGluIlePheLeuSerValThrAlaIleSerCysTyAsp 279
Db 1084 AACTTCAAGCGCTCTTTCACAGCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131

RESULT 14
US-09-016-434-750
; Sequence 750, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.434
```



```
QY 37 SerIleLeuPheLeuValValMetAsnThrArgSerValThrMetAlaValle 56
Db 328 TATGTGATCTCGCTACGCCAAGATGAAGACC-----GCTACCAACATCTACATCTCTA 381
QY 57 AsnLeuValValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeu 76
Db 382 AACCTGGCTATGTGTGATGAGCTGCTCATGCTCAGCGTGCCCTTCTGGTCACTCCACG 441
QY 77 IleLysLysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
Db 442 CTGTTGGCCACCTGGCCCTTCGGCGCGCTACTTTGGCCCTGGTGTCTCAGCGTGATGCG 501
QY 97 IleHisMetTyrLeuThrPheLeuPheTyrValValleLeuValThrArgTyrLeulle 116
Db 502 GTCACATGTTTCCACGACATCTACTGTCTGACTGTCTTAGTGTGGACCGCTATGTGGCT 561
QY 117 PhePheLysCysLysAspValValGluPheTyrArgLysLeuHisAlaValAlaAlaSer 136
Db 562 GTGGTGACCCGATCAAGCGACGCGCTACGCTGGCGCCCTGCTGGCGCAAGTAGTAGAAC 621
QY 137 AlaGlyMetTrpThrLeuValleValleValValProLeuValVal----SerArgTyr 155
Db 622 CTGGCGGTGGTGGCTGCTTACTTACTGCTATCTTGTGCTGCTGCTGCTGCTGCTGCTG 681
QY 156 GlyIleHisGluGluTyrAsnGluLysHisCysPheLysPheHisLysGluLeuAlaTyr 175
Db 682 GCACCCACACGAT---GGCACGCTAGCTGCTGACATGCTCATGCTGCGCGCGCCGACG 738
QY 176 ThrTyr---ValLysIleLeuAsnTyrMetIleValle---PheValleAlaValAla 193
Db 739 CGCTGGTGTGGCTGCTTACTTATACATTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTG 798
QY 194 ValIleLeuLeuValPheGlnValPheIleIleMetLeuMetValGlnLysLeuValHis 213
Db 799 GCCATTTGGCTGTGTAT-----GTGCTCATCATTCGCAAGATGCGC--- 840
QY 214 SerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsn----- 227
Db 841 --ATGGTGGCCCTCAAGCTGGCTGGCGAGCGCAAGCGCTCAGAGCGCAAGATCACT 897
QY 228 -----LeuPhePheIleGlyValleLeuValCysPheLeuProTyrGlnPhePhe 244
Db 898 CTATGTTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 951
QY 245 ArgIleTyrTyrLeuAsnVal----- 251
Db 952 GTGGTACAGCTGGTCAACGTGTTCCGCGAGCAAGCGCCAGCGCGTGGACGCTGCTCT 1011
QY 252 -----ValThrHisSerAsnAlaCysAsnSerLysValAlaPhe----- 264
Db 1012 GTCATCTCTGGCTATGCAACAGCTGTGCCAACCCCATCTCTACGGCTTCTCTGTCGGAC 1071
QY 265 --TyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAsp 279
Db 1072 AACTTCAGCGCTTTTCCAGCGCATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1119
```

RESULT 11

```
US-07-816-283-1
; Sequence 1, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911231
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-816-283-1
```

```
Alignment Scores:
Pred. No.: 5,08e-13 Length: 1634
Score: 218.00 Matches: 72
Percent Similarity: 45.89% Conservative: 73
Best Local Similarity: 22.78% Mismatches: 121
Query Match: 13.69% Indels: 50
DB: 14 Gaps: 14
```

US-10-055-106C-2 (1-305) x US-07-816-283-1 (1-1634)

```
QY 2 ProGlyHisAsnThrSerArgAsnSerSer---CysAspProIleValThrProHisLeu 20
Db 220 CCAGGGCGAATGCGTCCAGAACCGGACCTTGAGCGAGCGCCAGCGGCGCCACCTCTG 279
QY 21 IleSer---LeuTyrPheIleValleLeuIleGlyLeuValgly-----Valle 36
Db 280 ATCTCTTTCTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 339
QY 37 SerIleLeuPheLeuValLysMetAsnThrArgSerValThrThrMetAlaValle 56
Db 340 TAGTGTATCTCGCTATGCCAAGATGAAGACG-----GCCACCAACATCTACATCTTA 393
QY 57 AsnLeuValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeu 76
Db 394 ATCTGGCATTTGCTGATGATGCTGCTCATGCTCAGCGGCGCTTCTTAGTCACTCCACG 453
QY 77 IleLysLysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
Db 454 TTGTTGCGCACCTGGCCCTTCGCTGCGCTCTGCTGCGGCTCTGCTGCTGCTGCTGCTGCTG 513
QY 97 IleHisMetTyrLeuThrPheLeuPheTyrValValleLeuValThrArgTyrLeulle 116
Db 514 GTCAACATGTTTCCACGACATCTACTGTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 573
QY 117 PhePheLysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSer 136
Db 574 GTGGTGATCCCATCAAGCGCGCGCTACCGCGCGCCCGCCCGCGCCAGGCTAGTAAC 633
QY 137 AlaGlyMetTrpThrLeuValleValleValleValProLeuValVal----SerArgTyr 155
Db 634 CTGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 693
QY 156 GlyIleHisGluGluTyrAsnGluLysHisCysPheLysPheHisLysGluLeuAlaTyr 175
Db 694 GCGGCCAACAGCGAC---GGCACGCTGGCTTGCACATGCTCATGCCAGCGCCCTCAA 750
QY 176 ThrTyr---ValLysIleLeuAsnTyrMetIleValle---PheValleAlaValAla 193
Db 751 CGTGGCTGGTGGCTTCTGTTGTATACATTTCTCATGGGCTTCTGCTGCTGCTGCTGCTG 810
```

LENGTH: 1265 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA

US-07-816-283-3

Alignment Scores:
Pred. No.: 3 63e-13 Length: 1265
Score: 218.00 Matches: 72
Percent Similarity: 45.89% Conservative: 73
Best Local Similarity: 22.78% Mismatches: 121
Query Match: 13.69% Indels: 50
DB: Gaps: 14

US-10-055-106C-2 (1-305) x US-07-816-283-3 (1-1265)

Qy 2 ProGlyHisAsnThrSerArgAenSerSer---CysAspProIleValThrProHisLeu 20
Db 208 CTTGGACGAAGCGCTTCCAGAAATGCCATTAAAGCAAGGCAGAGGTAGCGCATTCCTC 267
Qy 21 IleSer---LeuTyrrPheIleValLeuLleGlyLeuValgly-----Vallie 36
Db 268 ATCTCTTTTCATCTACTCCGTTGGTGATGCTTGGTGGGACTGTGTGGAACTCTATGTCATC 327
Qy 37 SerIleLeuPheLeuValHisMetAanThraArgSerValThrMetAlaValille 56
Db 328 TATGTGATCCTCGGCTACGCCAAGATGAAGACC-----GCTACAACATCTACATTTCTA 381
Qy 57 AsnLeuValValHisValPheLeuLeuThrValPropheArgLeuThrTyrrLeu 76
Db 382 AACCTGGCTATTGCTCATGAGCTGCTCATGCTCAGCGTGCCTTTCTGTCTCACITCCACG 441
Qy 77 IleLySylThrTrpMetPheGlyLeuProPhCyLeYspHeValSerAlametLeuHls 96
Db 442 CTETTCGGCACATGCGCCCCCTTCGGCGGCTACTTTGGCCGCTGCTGCTCAGGTGGATCG 501
Qy 97 IleHisMetTyrrLeuthrPheLeuPheTyrrValIleLeuValThrArgTyrrLeulle 116
Db 502 GTCAACATGTTACCAGCATCTACTGCTGACTGTGCTTAGTGTGGACCGCTATGTGGCT 561
Qy 117 PhePheLYscyslysaspysvalgluPheTyrrgLyLeuHisAlavalalaalaser 136
Db 562 GTGGTGACCCGATCAAAGCAGCGCGCTACCGTGGCCCACTGTGGCCAAAGTAGTGAAc 621
Qy 137 AlaGlyMetTrpThrLeuValIleValIleValValproLeuValVal---SerArgTyrr 155
Db 622 CTGGCGGTGGGTGCTGTGCTATTACTGTTTATCTTGCCCATGCTGCTCTCTCACGCCACC 681
Qy 156 GlylleHisGlutyrAnslungluHuHlsCysPheLYspHeHlsGLyleuLaalyr 175
Db 682 GCAGCCAACAGCAT---GGCAGCGTAGCGTGCAACATGCTCATGCCGCCGCCCCCAG 738
Qy 176 ThrTyrr---VallylIleAenTyrrMetIleValille---PheValIleAlaValala 193
Db 739 CGTGGTGGTGGGCTCGCTTATACATACTTTCATGGGCTTCTGCTGCTGCTGGG 798
Qy 194 ValileLeuLeuValPheGlnValPheIlelleMetLeuMetValGlnLYserArghis 213
Db 799 GCCATTTCGCTGTATTAT-----GTGCTCATCATTTGCCAAGATGGC--- 840
Qy 214 SerLeuLeuSerHisGlnGlnPluPheTpAlaGlnLeuLYsaAsn----- 227
Db 841 ---ATGGTGCCCTCAAGCTGGCTGGCAGCAGCGCAAGGCTCAGAGCGCAAGATCACT 897
Qy 228 -----LeuPhePheIleGlyValIleLeuValCysPheLeuProTyrrGlnPhephe 244
Db 898 CTAATGTGTGATGATGGTGGTATTTTTGTTCATCTGTGGATGGCT-----TTCTAC 951
Qy 245 ArgIleTyrrXLeuAenVal----- 251
Db 952 CTCGTACACGCTGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011


```

;
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,103
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/816,283
; FILING DATE: 01-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1205 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1187
;
; US-08-417-103-13
;
; Alignment Scores:
; Pred. No.: 3,4e-13 Length: 1205
; Score: 218.00 Matches: 72
; Percent Similarity: 45.89% Conservative: 73
; Best Local Similarity: 22.78% Mismatches: 121
; Query Match: 13.69% Indels: 50
; DB: 1 Gaps: 14
;
; US-10-055-106C-2 (1-305) x US-08-417-103-13 (1-1205)
;
; Qy 2 ProGlyHisAsnThrSerArgAsnSerSer---CysAspProIleValThrProHisLeu 20
; Db 135 CCAGGCGGAATGCTCCAGAACGGGACCTTGAGCGAGGCGCCAGGCGGCCATCCTG 194
;
; Qy 21 IleSer---LeuTyrPheIleValleuIleGlyLeuValGly-----Valile 36
; Db 195 ATCTCTTTCACTACTCGGTGGTGGCTGTGGGGCTGTGGGAACCTCTATGGTCATC 254
;
; Qy 37 SerIleLeuPheLeuValIleValMetAsnThrArgSerValThrMetAlaValile 56
; Db 255 TACGTGATCCTCGCTATGCCAGATGAGAGC-----GCCACCAACATCTACATCCTA 308
;
; Qy 57 AsnLeuValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeu 76
; Db 309 AATCTGGCCATTGTGTGATGAGTGTCTCATGCTCAGCGTGCCTTCCTAGTCACTCCACG 368
;
; Qy 77 IleLysLysThrTyrMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
; Db 369 TTGTGGCCCACTGGCCCTTGGTGGCTGTCTGCGCCTCGTGCCTCAGCGTGGACGCG 428
;
; Qy 97 IleHisMetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeulle 116
; Db 429 GTCAACATGTTCCACGAGCATCTACTGTGTGCTGTGCTCAGCGTGGACCGCTAGTGGCC 488
;
; Qy 117 PhePheLysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSer 136
;
; Db 489 GTGGTGCATCCCATCAAGCGCGCCCGCTACCGCGGCCCCACCGTGGCCAAAGGTAGTAAAC 548
;
; Qy 137 AlaGlyMetTyrThrLeuValIleValIleValProLeuValVal---SerArgTyr 155
; Db 549 CTGGGCGGTGGTGGTCTATCGCTCGTCTCATCTCCGCCCATCGTGTCTTCTCTCGCACC 608
;
; Qy 156 GlyIleHisGluGluTyrAsnGluHisCysPheLysPheHisLysGluLeuAlaTyr 175
; Db 609 GCGGCCAACAGCGAC---GGCACGGTGGCTTGCACACATGCTCATGCCAGAGCCCGCTCAA 665
;
; Qy 176 ThrTyr---ValLysIleIleAsnTyrMetIleValIle---PheValIleAlaValAla 193
; Db 666 CGCTGGCTGGTGGCTTGTGTGTACACATTCTCATGGGCTTCTGCTGCCCGTGGGG 725
;
; Qy 194 ValIleLeuValPheIleValPheIleLeuMetLeuMetValGlnLysLeuArgHis 213
; Db 726 GCTATCTGCTGTGTCTAC-----GTGCTCATCATTTGCTAAGATGCGC--- 767
;
; Qy 214 SerLeuLeuSerHisGlnGluPheTyrAlaGlnLeuLysAsn----- 227
; Db 768 ---ATGGTGGCCCTCAAGCGCGCTGGCAGCAGCGCCAGCGCTCGAGGGCGAAGATCACC 824
;
; Qy 228 -----LeuPhePheIleGlyValIleLeuValCysPheLeuProTyrGlnPhePhe 244
; Db 825 TTAATGGTGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 878
;
; Qy 245 ArgIleTyrTyrLeuAsnVal----- 251
; Db 879 GTGGTGCAGCTGGTTAACTGTTTCTGAGCAGGAGCAGCGCCACCGTGTCTATGGCTTCTCTCAGAC 938
;
; Qy 252 -----ValThrHisSerAsnAlaCysAsnSerLysValAlaPhe----- 264
; Db 939 GTCACTCTGGCTATGCCAACAGCTGGCGCAACCCCATCTCTATGGCTTCTCTCAGAC 998
;
; Qy 265 ---TyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAsp 279
; Db 999 AACTTCAGCGCTCTTTCCACGCGATCTATGCTCATGCTGATGGAC 1046
;
; RESULT 9
; US-07-816-283-3
; Sequence 3, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOVATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816,283
; FILING DATE: 19911231
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

```

```

Db      214 ATATGACTTACCTTTCGAATGTTTATATGCAAAAGATGCATGGCCATTTGGAGAG 273
Qy      86 ProPheCysLysPheValSerAlaMetLeuHisIleHisValThrPheLeuPhe 105
Db      274 TACTTCTGCCAGATTATGGAGCTCTCACAGTGTCTTTTACCAAGCATTTCTTTATGGCTT 333
Qy      106 TyrValIleLeuValThrArgTyrLeuIlePhePheCysLysAspLysValGlu 125
Db      334 CTTCCTTTATAGTGTGACATACATAGCCGATGTACAGCCGAGTACGCCAAGAA 393
Qy      126 PheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetThrPheLeuValIleVal 145
Db      394 CTTAAACACAGCTGCAAGCGCTGCTGGAGTGTGAGATGCTGGAATATGACCTGACC 453
Qy      146 IleValValProLeuValSerArgTyrGlyIleHisGluGluTyrAsnGluHis 165
Db      454 ACGACACCTCTGCTGCTATGCTCTATAAGACCCAGATAAGATCCACTCCGCCACC 513
Qy      166 CysPheLysPheHisLysGluLeuAlaTyrThrTyrValIleHisValThrPheLeu 185
Db      514 TGCCTCAAGATTCTGACATCATC-----TATCTAAAGCTGTGAACGTGCTGAAC 564
Qy      186 ValIlePheValIleAlaValAlaValIleLeuValPheGlnValPheIleIleMet 205
Db      565 CTCACTCGATGACATTTTCTTCTGATTCCTTCTCATCATGATGGGTGCTACTTG 624
Qy      206 LeuMetValGlnLysLeuArgHisSerLeuSerHisGlnGluPheTrpAlaGlnLeu 225
Db      625 GTCAATTATATAATCTCTTCAAGCAGGAGCTCTTAAGCTGAACCCCAAGTCGAAGG 684
Qy      226 LysAsnLeuPhePheIleGlyVal-----IleLeuValCysPheLeuProTyr 241
Db      685 AAGTCCATAGGATCATCATCAGCTGTGGTGGAGGTGCTGCTGCTTTATGCCCTTC 744
Qy      242 GlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSerLys 261
Db      745 CACATCTGT---TTGCTTCTGATGCTGGGACCGGGGAGACAGTTACATCCCTGG 801
Qy      262 ValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeuLeu 281
Db      802 GGAGCCTTT-----ACCACCTTCTCTC---ATGAACCTCAGCAGCGTCTGGATGTGATT 852
Qy      282 LeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeu 298
Db      853 CTCTAC---TACATCGTTTCAAAACAATTTTCAGGCTCGAGTCATTAGTGTC 900

RESULT 7
US-09-170-496D-35
; Sequence 35, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-35

Alignment Scores:
Pred. No.: 1,65e-13 Length: 996
Score: 220.00 Matches: 68
Percent Similarity: 44.11% Conservative: 63
Best Local Similarity: 22.90% Mismatches: 154
Query Match: 13.82% Indels: 12

```

```

Db      214 ATATGACTTACCTTTCGAATGTTTATATGCAAAAGATGCATGGCCATTTGGAGAG 273
Qy      6 ThrSerArgAsnSerSerCysAspProIleValThrProHisLeuIleSerLeuTyrPhe 25
Db      34 ACITTTAACAGCTCACATCCAGATGAATAACAAATATGCAGCCCTTGTCTCTATAGCTGT 93
Qy      26 IleValLeuIleGlyLeuValGlyValIleSerIleLeuPheLeuLeuValIleMet 45
Db      94 ATCTTCAATATGATATTTTGTAAACATCATCTGATTTGAGTTTTCAGTTGTACCCACC 153
Qy      46 AsnThrArgSerValThrMetAlaValIleAsnLeuValValHisSerValPhe 65
Db      154 AAGAAGAGAACACGCGTAAACCATCTATATGATGAATGTGGCATTAGTAGGACTTGATATTT 213
Qy      66 LeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThrTrpMetPheGlyLeu 85
Db      214 ATATGACTTTCCTCTTTCGAATGTTTATATGCAAAAGATGCATGGCCATTTGGAGAG 273
Qy      86 ProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyrLeuThrPheLeuPhe 105
Db      274 TACTTCTGCCAGATTATGGAGCTCTCACAGTGTCTTACCAAGCATTTCTTTATGGCTT 333
Qy      106 TyrValValIleLeuValThrArgTyrLeuIlePhePheLysCysLysAspLysValGlu 125
Db      334 CTTCCTTTTATAGTGTGACATGATACATGGCCATTTGACCCGAGTACGCCAAGAA 393
Qy      126 PheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetThrPheLeuValIleVal 145
Db      394 CTTAAACACAGCTGCAAGCGCTGCTGGAGTGTGAGATGCTGGAATATGACCTGACC 453
Qy      146 IleValValProLeuValSerArgTyrGlyIleHisGluGluTyrAsnGluHis 165
Db      454 ACGACACCTCTGCTGCTATGCTCTATAAGACCCAGATAAGATCCACTCCGCCACC 513
Qy      166 CysPheLysPheHisLysGluLeuAlaTyrThrTyrValIleHisIleAsnTyrMetIle 185
Db      514 TGCCTCAAGATTCTGACATCATC-----TATCTAAAGCTGTGAACGTGCTGAAC 564
Qy      186 ValIlePheValIleAlaValAlaValIleLeuValPheGlnValPheIleIleMet 205
Db      565 CTCACTCGATGACATTTTCTTCTGATTCCTTCTCATCATGATGGGTGCTACTTG 624
Qy      206 LeuMetValGlnLysLeuArgHisSerLeuSerHisGlnGluPheTrpAlaGlnLeu 225
Db      625 GTCAATTATATAATCTCTTCAAGCAGGAGCTCTTAAGCTGAACCCCAAGTCGAAGG 684
Qy      226 LysAsnLeuPhePheIleGlyVal-----IleLeuValCysPheLeuProTyr 241
Db      685 AAGTCCATAGGATCATCATCAGCTGTGGTGGAGGTGCTGCTGCTTTATGCCCTTC 744
Qy      242 GlnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSerLys 261
Db      745 CACATCTGT---TTGCTTCTGATGCTGGGACCGGGGAGACAGTTACATCCCTGG 801
Qy      262 ValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeuLeu 281
Db      802 GGAGCCTTT-----ACCACCTTCTCTC---ATGAACCTCAGCAGCGTCTGGATGTGATT 852
Qy      282 LeuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeu 298
Db      853 CTCTAC---TACATCGTTTCAAAACAATTTTCAGGCTCGAGTCATTAGTGTC 900

RESULT 8
US-08-417-103-13
; Sequence 13, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS

```

RESULT 6

US-09-016-434-1064

Sequence 1064, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELEPHONE: (650) 855-0555

TELEPHONE: (650) 845-4166

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1064:

SEQUENCE CHARACTERISTICS:

LENGTH: 993 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: GI066730

US-09-016-434-1064

Alignment Scores:

Pred. No.: 1,65e-13

Score: 220.00

Length: 993

Matches: 68

Percent Similarity: 44.11%

Conservative: 63

Best Local Similarity: 22.90%

Mismatches: 154

Query Match: 13.82%

Indels: 12

DB: 4

Gaps: 6

US-10-055-106C-2 (1-305) x US-09-016-434-1064 (1-993)

Qy 6 ThrSerArgAsnSerSerCysAspProIleValThrProHisLeuIleSerLeuTyrPhe 25

Db 34 ACTTTAAACAGCTCACATCCAGTGAATACAAAATGCAGCCCTTGCTCTTATAGCTGT 93

Qy 26 IleValLeuIleGlyLeuValGlyValIleSerIleLeuPheLeuValIleMet 45

Db 94 ATCTTCATTAATGGATATTATTTGAACATCACTGATTTGGTTTTCAGTTGTACCACC 153

Qy 46 AsnThrArgSerValThrThrMetAlaValIleAsnLeuValValHisSerValPhe 65

Db 154 AAGAAGAACCAACCGTAACCATCTATATGATGAATGTGGCAATTAGTACATTATTT 213

Qy 66 LeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThrTyrMetPheGlyLeu 85

Db 1130 ---TTTAAGGACACACTA 1144

Alignment Scores:

Pred. No.: 1.28e-13

Score: 223.00

Length: 1401

Matches: 70

Percent Similarity: 46.41%

Conservative: 72

Best Local Similarity: 22.88%

Mismatches: 136

Query Match: 14.01%

Indels: 28

DB: 4

Gaps: 11

US-10-055-106C-2 (1-305) x US-09-585-876-1 (1-1401)

Qy 4 HisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeuIleSerLeu 23

Db 269 AATAACAACAGCAGCACTGCACATTTGAAAATCTCAAGACAGAGATTTTCCCAATGTA 328

Qy 24 TyrPheIleValLeuIleGlyLeuValGly---ValIleSerIleLeuPheLeu 42

Db 329 TATCTGATAATATTTTCTGGGGAGCTCTGGGAAATGGGTGTCCATATATGTTTCTCTG 388

Qy 43 ValIleMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValValHis 62

Db 389 CAGCCTTATAAGAGTCCACATCTGTGAACGTTTTCATGCTAAATCTGGCCATTCAGAT 448

Qy 63 SerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLys---LysThrTyr 81

Db 449 CTCCTCTTCATAAGCAGCTGCTCCCTCAGGCTGCTATATCTTAGAGGCTCCAGTTGG 508

Qy 82 MetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyrLeu 101

Db 509 ATATTTGGAGACCTGGCCCTGCAGGATTATGCTTATCTTGTATGTCAACATGTACAGC 568

Qy 102 ThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePheLysCysLys 121

Db 569 AGTATTATTTCTGACCCGCTGCTGAGTGTGTGCGCTTCTGCGCAATG----- 616

Qy 122 AspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTyrPhe 141

Db 617 -----GTTCACCCCTTTGGCTTTCGAT---GTCCACGAGCATGAGGTGCTGGATC 667

Qy 142 LeuValIleValIleValValProLeuValValSerArgTyrGlyIleHisGluLeuTyr 161

Db 668 CTCTGTGGGATCATATGATGCTTATCATGGCTTCTCAATAATGCTCTGACAGATGGC 727

Qy 162 AsnGluGlu-----HisCysPheLysPheHisLys 171

Db 728 TCTGACGACGACGAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAATGCTTAAG 787

Qy 172 GluLeuAlaTyrThrTyrValIys---IleIleAsnTyrMetIleValIlePheValIle 190

Db 788 CTCGACACCATGAATATATTTGGCTGGTGGGGCTGCTGCTGCCATTTTTCACATC 847

Qy 191 AlaValAlaValIleLeuValPheGlnValPheIleIleMetLeuMetValGlnLys 210

Db 848 AGCATCTGTATCTGTGTGATCATTCGGGTCTGTAAAAGTGGAGGTCCCAAGTCGGGG 907

Qy 211 LeuArgHisSerLeuLeuSerHisGlnGluPheTyrAlaGlnLeuLysAsnLeuPhePhe 230

Db 908 CTGCGG-----GTTCTTCACAGAG-----GCACTACCCACCATCATCATCACC 952

Qy 231 IleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIleTyrTyrLeuAsn 250

Db 953 TTGATCATCTCTCTTCTGTTCTGCTGCTGCTATCACAACACTGATTAAGCTTGTGATCATCTG 1009

Qy 251 ValValThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsnGluIlePheLeu 270

Db 1010 ACGACATGGAAGTGGGTTTATCAAGACAGACTGCATAAAGCTTGTGTTATCATCTG 1069

Qy 271 SerValThrAlaIle---SerCysTyrAspLeuLeuPheValPheGlyGlySerHis 289

Db 1070 GTCTTGGCAGCAGCAATGCTGCTGCTCAATCTCTGCTCTTACTTGTCTGCGGAGAT 1129

Qy 290 TrpPheLysGlnLysIle 295

Db 1130 ---TTTAAGGACACACTA 1144

```
Db 991 TGTACATAGCCATA-----TCAGGTACATCCCAAAATCCAGC 1029
Qy 219 GlnGluPheTrpAlaGlnLeuLysAsn-----LeuPhePhe 230
Db 1030 AGGCAATTCAATGTCAGTCAAGCGGAAAGCGAAACATAACCCAGAGCATCAGGGTGTGT 1089
Qy 231 IleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIle----- 246
Db 1080 GTGGGTGTGTATTTTACCTGCTTTTACCATATACATCTGTGCGAGATGCCCTTCTACTTTT 1149
Qy 247 TyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSerLysValAlaPheTyr--- 265
Db 1150 AGTCACCTTAGACAGCGCTTTTAGATCAATCTGCA-----CAAAAAATCTATATTACTGC 1203
Qy 266 AsnGluIlePheLeuSerValThrAlaIleSer---CysTyrAspLeuLeuVal 284
Db 1204 AAAGAAATACACTTTTCTGTCTGCGTGAATGTTTSCCTGGATCCCAATATTACTTT 1263
Qy 285 Phe-----GlyGlySerHisTrpPheLysGlnLys 294
Db 1264 TTCATGTGTAGTCAATTTTCAAGATGGCTGTTCAAAAAA 1302

RESULT 4
US-09-919-172-21
; Sequence 21, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1650519CB1
US-09-919-172-21

Alignment Scores:
Pred. No.: 2,03e-14 Length: 1444
Score: 231.00 Matches: 76
Percent Similarity: 43.13% Conservative: 59
Best Local Similarity: 24.28% Mismatches: 144
Query Match: 14.51% Indels: 34
DB: 4 Gaps: 10

US-10-055-106C-2 (1-305) x US-09-919-172-21 (1-1444)
Qy 2 ProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeuIle 21
Db 406 CCAGGAAGAACACACACCTTCAAGATTTGACACATTTGCTTGGCGGTCTTAT 465
Qy 22 SerLeuTyrPheIle-----ValLeuIleGlyLeuValGlyValIleSerIleLeu 39
Db 466 CTCATTATATTGTGGCAAGCATCTTGTCTGAATGGTTTAGCA-----GTG 510
Qy 40 PheLeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuVal 59
Db 511 TGGATCTCTTCACATAGGATATACACAGCTTCATATCTTCTCAAAACATAGTG 570
Qy 60 ValValHisSerValPheLeuThrValProPheArgLeuThrTyrLeuLys--- 78
Db 571 GTTCGACACCTCATATGACGCTGACATTTCCATTTTCGAATAGTCCATGATGAGGATTT 630
```

```
Qy 79 LysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHis 98
Db 631 GGACCTTGGTACTCAAGTTTATTTCTGCAGATACACTTTCAGTTTGTGTTTATGCAAC 690
Qy 99 MetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePhe 118
Db 691 ATGTATACTTCCATCGTGTCTTGGCTGATAGCAATGATCGCTATCTGAAGGTGGTC 750
Qy 119 LysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGly 138
Db 751 AAGCCATTTGGGACATCTCGGATGTACAGCATAACCTTCACGAAGGTTTTATCTGTTGT 810
Qy 139 MetTyrThrLeuValIleValValValProLeuValValSerArgTyrGlyIleHis 158
Db 811 GTTGGGTGATCACTGCTGTTTGTGCGCGTGTCTGTGATTCGATCGGA 870
Qy 159 GluGluTyrAsnGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrVal 178
Db 871 ACAGAGGACAATATCCATGACTCTCAAAACTTAAAGTCTTTTGGGGGTCAAAATGGCAT 930
Qy 179 LysIleIleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuVal 198
Db 931 ACGGCAGTCACCTATGTGAACAGCTGCTGTTTGTGCGCGTGTCTGTGATTCGATCGGA 990
Qy 199 PheGlnValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuSerHis 218
Db 991 TGTACATAGCCATA-----TCCAGGTACATCCCAAAATCCAGC 1029
Qy 219 GlnGluPheTrpAlaGlnLeuLysAsn-----LeuPhePhe 230
Db 1030 AGGCAATTCAATGTCAGTCAAGCGGAAAGCGAAACATAACCCAGAGCATCAGGGTGTGT 1089
Qy 231 IleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIle----- 246
Db 1090 GTGGCTGTGTATTTTACCTGCTTTTACCATATACATCTGTGCGAGATGCCCTTCTACTTTT 1149
Qy 247 TyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSerLysValAlaPheTyr--- 265
Db 1150 AGTCACCTTAGACAGCGCTTTTAGATGAATCTGCA-----CAAAAAATCTTATATTACTGC 1203
Qy 266 AsnGluIlePheLeuSerValThrAlaIleSer---CysTyrAspLeuLeuVal 284
Db 1204 AAAGAAATACACTTTTCTGTCTGCGTGAATGTTTSCCTGGATCCCAATATTACTTT 1263
Qy 285 Phe-----GlyGlySerHisTrpPheLysGlnLys 294
Db 1264 TTCATGTGTAGTCAATTTTCAAGATGGCTGTTCAAAAAA 1302

RESULT 5
US-09-585-876-1
; Sequence 1, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 43239, A No. 6586205e1 GPCR-Like Molecule and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 5800-88
; CURRENT APPLICATION NUMBER: US/09/585,876
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: 60/182,061
; EARLIER FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)...(1237)
US-09-585-876-1
```

Qy 97 IleHisMetTyrLeuThrPheLeuPheTyrValValleLeuValThrArgTyrLeulle 116
Db 779 GTCAACCTCTATTGTAGCATCTTCTTTATGACAGCC-----ATGAGC 820
Qy 117 PhePheLysCys-----LysAspLysValGluPheTyrArgLysLeu 130
Db 821 TTTTTCGGTGCATGCAATGTTTTCAGTCAGACATATATTTGGTTACACAGAA 880
Qy 131 HisAlaValAlaAlaSerAlaGlyMetTyrThrLeuValleValleValProLeu 150
Db 881 AAAGCCAGGTTGTGTGTGTAGTATTTGGATTTTGTGATTTTGACCAATTT 940
Qy 151 ValValSerArgTyrGlyLeHisGluTyrAnGluHisCysPheLysPheHis 170
Db 941 CTAATGGCCAAA---CCCAAAAGATGGGAAATAATACCAAGTCTTTGACCCCA 997
Qy 171 LysGlu---LeuAlaTyrThrTyrValLysleleleleTyr-----MetileValle 187
Db 998 CAAGCAATCAAACTAAATAATCATGTTTGTCTTGTGATTTATGTCATTTGTTTGGC 1057
Qy 188 PheValleAlaValAlaValleLeuValPheGlnValPheleleleMetLeuMet 207
Db 1058 TTTATCATCCCTTTTGTATTATATATGTCGTACACATGATCAATTTGACCTTACTA 1117
Qy 208 ValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTyrAlaGlnLysAsn 227
Db 1118 AAAAAATCAATGAAAAAATCTGCAAGTCATAAAAGGCTATAGGAATGATC----- 1171
Qy 228 LeuPhePheleleGlyValleLeuValCysPheLeuProTyrGlnPhePheArgIleTyr 247
Db 1172 ATGGTCGTGACCGTCCTTTTATGTCATGTTTCATGTCATATATTTCAACGACCAT 1231
Qy 248 TyrLeuAnValVal---ThrHisSerAnAlaCysAsnSerLysValAlaPheTyrAsn 266
Db 1232 CACCTTCATTTTACACAAATGAACTAAACCTGTGATTTCTGCTTGAATGACAGAG 1291
Qy 267 GluilePheLeuSerValThrAlaIleSer-----CysTyrAspLeuLeuPhe 283
Db 1292 TCCGTGGTCATAACCTGTCTCTGCTGTCATCAATTTGTTGTTGACCTCTCTCTAT 1351
Qy 284 ValPheGlyGlySerHisTyrPheLysGln 293
Db 1352 TTCCTTTCTGGGGTAACTTTAGGAAGAAG 1381

RESULT 3
US-08-988-876-4
Sequence 4, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
Filing Date: Herewith
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1444 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1650519
US-08-988-876-4

Alignment Scores:
Pred. No.: 2,03e-14 Length: 1444
Score: 231.00 Matches: 76
Percent Similarity: 43.13% Conservative: 59
Best Local Similarity: 24.28% Mismatches: 144
Query Match: 14.51% Indels: 34
DB: 10 Gaps: 10

US-10-055-106C-2 (1-305) x US-08-988-876-4 (1-1444)

Qy 2 ProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeulle 21
Db 406 CCAGGAAGAACACCCCTTCAATGAATTTGACACAAATGCTTGGCGGCTTTAT 465
Qy 22 SerLeuTyrPheIle-----ValleuileGlyLeuValGlyValleSerIleLeu 39
Db 466 CTATATATTTTGGCAGCATCTTGTGAATGGTTAGCA-----GTG 510
Qy 40 PheLeuLeuValLysMetAsnThrArgSerValThrMetAlaValleLeuVal 59
Db 511 TGGATCTTCTCCACATTTAGGAATAAACACCGCTTCATATTTCTATCTCAAAAACATAGT 570
Qy 60 ValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeulleLys-- 78
Db 571 GTTGACAGCTCATATGACGCTGACATTTCCATTTGCAATAGTCCATGATGAGGATTT 630
Qy 79 LysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 98
Db 631 GGACCTTGGTACTTCAAGTTTATTTCTCTGCAGATACACTTCACTTTTGTATGCAAA 690
Qy 99 MetTyrLeuThrPheLeuPheTyrValValleLeuValThrArgTyrLeullePhePhe 118
Db 691 ATGTATATCTTCCATCGGTTCCTTGGGCTGATAGCATGATGCTATCTGAAGTGGTC 750
Qy 119 LysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGly 138
Db 751 AAGCATTTGGGACTCTCGGATGTACAGCATAACCTTCACGAAGGTTTATCTGTGT 810
Qy 139 MetTrpThrLeuValleValleValleValProLeuValValSerArgTyrGlyLeHis 158
Db 811 GTTTGGGTGATCATGCTGTTTGTCTTCCAAAACATCATCTCTGCAAAATGTCAGCCA 870
Qy 159 GluGluTyrAnGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrVal 178
Db 871 ACAGGACATATATCCATGATCTCAAAACTTAAAGTCTTTGGGGTCAAAATGSCAT 930
Qy 179 LysleleleAsnTyrMetIleVallePheValleleAlaValleLeuLeuVal 198
Db 931 ACGGAGTCACCTATGTGAACAGCTGCTTGTGTGGCCGCTGCTGATTTCTGATCGGA 990
Qy 199 PheGlnValPheIleleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHis 218

```
/ REFERENCE/DOCKET NUMBER: GH-70001-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5219
/ TELEFAX: 610-270-5090
/
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1578 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-09-044-404A-1

Alignment Scores:
Pred. No.: 2,76e-15 Length: 1578
Score: 240.00 Matches: 67
Percent Similarity: 48.06% Conservative: 82
Best Local Similarity: 21.61% Mismatches: 133
Query Match: 15.08% Indels: 28
DB: 3 Gaps: 11

US-10-055-106C-2 (1-305) x US-09-044-404A-1 (1-1578)
QY 3 GlyHisAsnThrSerArgAsnSerSerCys-----AspProIleValThrPro 18
DB 479 GGAATCTGCACAGTATCTCTGCGCATGCCATGACACTATTGATGACTTCGCGCAATCAA 538
QY 19 HisLeuIleSerLeuThrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIle 38
DB 539 GTGTATTCACCTTGACTGATGATCTCTGTGTAGGCTCTTGTGGCAATGCGCTTTGTG 598
QY 39 LeuPheLeuValLys---MetAsnThrArgSerValThrMetAlaValIleAsn 57
DB 599 CTCTATGCTCATATAAAACCTATCACAAGAGTCAGCCTTCCAAAGTATACATGATTAAT 658
QY 58 LeuValValValHisSerValPheLeuThrValProPheArgLeuThrTyrLeuIle 77
DB 659 TTAGCAGTAGCAGATCTACTTTGTGTGGCAGACTGCTCTCCGTGTGGTCTATATGTC 718
QY 78 LysLys---ThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
DB 719 CACAAAGGCATTGTCCTTTGTGTGACTCTCTGTGGCGCCTCAGCACCTATGCTTTGTAT 778
QY 97 IleHisMetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIle 116
DB 779 GTCAACCTCTATTGTAGCATCTCTTTATGACAGCC-----ATGAGC 820
QY 117 PhePheLysCys-----LysAspLysValGluPheTyrArgLysLeu 130
DB 821 TTTTCCGGTGCAATGCAATGTTTTCAGTCCAGAACATTAATTTGGTTACACAGAA 880
QY 131 HisAlaValAlaAlaSerAlaGlyMetTrpThrLeuValIleValIleValValProLeu 150
DB 881 AAAGCCAGGTTTGTGTGTGTAGTATTTGGATTTTGTGATTTTGTACCAAGTCTCCATTT 940
QY 151 ValValSerArgTyrGlyIleHisGluGluTyrAsnGluHisCysPheLysPheHis 170
DB 941 CTAATGGCCAA---CCACAAAGATGGGAAATAATACCAAGTCTTGAGCCCA 997
QY 171 LysGlu---LeuAlaTyrThrTyrValLysIleIleAsnTyr-----MetIleValIle 187
DB 998 CAAGCAATCAAACTAAAAATCATGTTTGTGTCTTCATTTGTCATTTGTTGTGTC 1057
QY 188 PheValIleAlaValAlaValIleLeuValPheGlnValPheIleIleMetLeuMet 207
DB 1058 TTTATCATCCCTTTGTTATTAATTTGTTGTGTGTACATGATCATTTGACCTTACTA 1117
QY 208 ValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsn 227
DB 1118 AAAAAATCAATGAAAAAATCTGTCAAGTCATATAAAAGGCTATAGGAATGATC----- 1171
QY 228 LeuPhePheIleGlyValIleLeuValCysPheLeuProTyrGlnPheArgIleTyr 247

REFERENCE/DOCKET NUMBER: GH-70001-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5219
/ TELEFAX: 610-270-5090
/
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1578 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-09-044-404A-1

Alignment Scores:
Pred. No.: 2,76e-15 Length: 1578
Score: 240.00 Matches: 67
Percent Similarity: 48.06% Conservative: 82
Best Local Similarity: 21.61% Mismatches: 133
Query Match: 15.08% Indels: 28
DB: 3 Gaps: 11

US-10-055-106C-2 (1-305) x US-09-044-404A-1 (1-1578)
QY 3 GlyHisAsnThrSerArgAsnSerSerCys-----AspProIleValThrPro 18
DB 479 GGAATCTGCACAGTATCTCTGCGCATGCCATGACACTATTGATGACTTCGCGCAATCAA 538
QY 19 HisLeuIleSerLeuThrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIle 38
DB 539 GTGTATTCACCTTGACTGATGATCTCTGTGTAGGCTCTTGTGGCAATGCGCTTTGTG 598
QY 39 LeuPheLeuValLys---MetAsnThrArgSerValThrMetAlaValIleAsn 57
DB 599 CTCTATGCTCATATAAAACCTATCACAAGAGTCAGCCTTCCAAAGTATACATGATTAAT 658
QY 58 LeuValValValHisSerValPheLeuThrValProPheArgLeuThrTyrLeuIle 77
DB 659 TTAGCAGTAGCAGATCTACTTTGTGTGGCAGACTGCTCTCCGTGTGGTCTATATGTC 718
QY 78 LysLys---ThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
DB 719 CACAAAGGCATTGTCCTTTGTGTGACTCTCTGTGGCGCCTCAGCACCTATGCTTTGTAT 778
QY 97 IleHisMetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIle 116
DB 779 GTCAACCTCTATTGTAGCATCTCTTTATGACAGCC-----ATGAGC 820
QY 117 PhePheLysCys-----LysAspLysValGluPheTyrArgLysLeu 130
DB 821 TTTTCCGGTGCAATGCAATGTTTTCAGTCCAGAACATTAATTTGGTTACACAGAA 880
QY 131 HisAlaValAlaAlaSerAlaGlyMetTrpThrLeuValIleValIleValValProLeu 150
DB 881 AAAGCCAGGTTTGTGTGTGTAGTATTTGGATTTTGTGATTTTGTACCAAGTCTCCATTT 940
QY 151 ValValSerArgTyrGlyIleHisGluGluTyrAsnGluHisCysPheLysPheHis 170
DB 941 CTAATGGCCAA---CCACAAAGATGGGAAATAATACCAAGTCTTGAGCCCA 997
QY 171 LysGlu---LeuAlaTyrThrTyrValLysIleIleAsnTyr-----MetIleValIle 187
DB 998 CAAGCAATCAAACTAAAAATCATGTTTGTGTCTTCATTTGTCATTTGTTGTGTC 1057
QY 188 PheValIleAlaValAlaValIleLeuValPheGlnValPheIleIleMetLeuMet 207
DB 1058 TTTATCATCCCTTTGTTATTAATTTGTTGTGTGTACATGATCATTTGACCTTACTA 1117
QY 208 ValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsn 227
DB 1118 AAAAAATCAATGAAAAAATCTGTCAAGTCATATAAAAGGCTATAGGAATGATC----- 1171
QY 228 LeuPhePheIleGlyValIleLeuValCysPheLeuProTyrGlnPheArgIleTyr 247

GENERAL INFORMATION: GANESH M.
APPLICANT: SATHE, WENDY
APPLICANT: HALSEY, WENDY
APPLICANT: ELLIS, CATHERINE E.
APPLICANT: AVES, ROBERT S.
APPLICANT: FOLEY, JAMES J.
APPLICANT: SARAU, HENRY M.
APPLICANT: CHAMBERS, JON
TITLE OF INVENTION: CDNA CLONE HMTF81 THAT ENCODES A NOVEL
FILE REFERENCE: GH-70001-1D1
CURRENT APPLICATION NUMBER: US/09/586,924
CURRENT FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 09/044,404
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 08/844,795
PRIOR FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1578
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-586-924-1

Alignment Scores:
Pred. No.: 2,76e-15 Length: 1578
Score: 240.00 Matches: 67
Percent Similarity: 48.06% Conservative: 82
Best Local Similarity: 21.61% Mismatches: 133
Query Match: 15.08% Indels: 28
DB: 4 Gaps: 11

US-10-055-106C-2 (1-305) x US-09-586-924-1 (1-1578)
QY 3 GlyHisAsnThrSerArgAsnSerSerCys-----AspProIleValThrPro 18
DB 479 GGAATCTGCACAGTATCTCTGCGCATGCCATGACACTATTGATGACTTCGCGCAATCAA 538
QY 19 HisLeuIleSerLeuThrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIle 38
DB 539 GTGTATTCACCTTGACTGATGATCTCTGTGTAGGCTCTTGTGGCAATGCGCTTTGTG 598
QY 39 LeuPheLeuValLys---MetAsnThrArgSerValThrMetAlaValIleAsn 57
DB 599 CTCTATGCTCATATAAAACCTATCACAAGAGTCAGCCTTCCAAAGTATACATGATTAAT 658
QY 58 LeuValValValHisSerValPheLeuThrValProPheArgLeuThrTyrLeuIle 77
DB 659 TTAGCAGTAGCAGATCTACTTTGTGTGGCAGACTGCTCTCCGTGTGGTCTATATGTC 718
QY 78 LysLys---ThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
DB 719 CACAAAGGCATTGTCCTTTGTGTGACTCTCTGTGGCGCCTCAGCACCTATGCTTTGTAT 778
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 25, 2004, 20:06:25 ; Search time 87 Seconds

(without alignments)
1945.517 Million cell updates/sec

Title: US-10-055-106C-2

Perfect score: 1592

Sequence: 1 MPCHNTSRNSSCDIVTPHL.....GGSHWFQKIGLWNCVLCR 305

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO.spool/US10055106/runat.21042004.161132.26207/app.query.fasta.1.455
-DB=Issued Patents NA -QFWT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10055106 @CGN.1.1.56 @runat.21042004.161132.26207 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240	15.1	1578	3	US-09-044-404A-1
2	240	15.1	1578	4	US-09-586-924-1
3	231	14.5	1444	3	US-08-988-876-4
4	231	14.5	1444	4	US-09-919-172-21
5	223	14.0	1401	4	US-09-585-876-1
6	220	13.8	993	4	US-09-016-434-1064
7	220	13.8	996	4	US-09-170-496D-35
8	218	13.7	1205	1	US-08-417-103-13
9	218	13.7	1265	1	US-07-816-283-3
10	218	13.7	1265	1	US-08-417-103-3
11	218	13.7	1634	1	US-07-816-283-1
12	218	13.7	1634	1	US-08-417-103-1

ALIGNMENTS

RESULT 1

US-09-044-404A-1
; Sequence 1, Application US/09044404A
; Patent No. 6200775
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: AMES, ROBERT
; APPLICANT: FOLEY, JAMES
; APPLICANT: SARAU, HENRY
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 790 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,404A
; FILING DATE: MARCH 19, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,795
; FILING DATE: APRIL 22, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T.
; REGISTRATION NUMBER: 34,344

Sequence 1302, Ap
Sequence 750, App
Sequence 7, Appli
Sequence 7, Appli
Sequence 11, Appl
Sequence 169, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 1479, Ap
Sequence 181, App
Sequence 183, App
Sequence 1270, Ap
Sequence 1484, Ap
Sequence 1484, Ap
Sequence 43, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appl
Sequence 46, Appl
Sequence 1190, Ap
Sequence 1021, Ap
Sequence 1, Appli
Sequence 1247, Ap
Sequence 1, Appli
Sequence 1426, Ap
Sequence 31, Appl
Sequence 7, Appli
Sequence 1, Appli
Sequence 717, App

13 218 13.7 1634 4 US-09-016-434-1302
14 217 13.6 1140 4 US-09-016-434-750
15 217 13.6 1301 2 US-08-467-948A-7
16 217 13.6 1301 3 US-08-467-948A-7
17 214 13.4 987 4 US-09-170-496D-11
18 214 13.4 987 4 US-09-170-496D-169
19 214 13.4 1027 3 US-09-303-524A-1
20 214 13.4 1054 1 US-08-148-215A-1
21 214 13.4 1596 4 US-09-016-434-1479
22 214 13.4 2416 4 US-09-016-434-1270
23 213 13.4 996 4 US-09-170-496D-183
24 211 13.3 1020 4 US-09-170-496D-181
25 208.5 13.1 1900 4 US-09-016-434-1484
26 208.5 13.1 1901 1 US-08-153-848-43
27 208.5 13.1 1901 3 US-09-299-843A-43
28 208.5 13.1 1901 4 US-09-088-337B-43
29 208.5 13.1 1901 5 PCT-US93-11153-43
30 208.5 13.1 2453 5 PCT-US95-07180-1
31 208 13.1 1143 1 US-08-467-125-1
32 208 13.1 1143 2 US-08-911-320A-1
33 208 13.1 1143 3 US-09-217-101-1
34 208 13.1 1842 4 US-09-016-434-46
35 206.5 13.0 1495 4 US-09-016-434-1190
36 206.5 13.0 1495 4 US-09-023-655-1021
37 206.5 13.0 2156 1 US-08-012-988A-1
38 206.5 13.0 2156 4 US-09-023-655-1247
39 205 12.9 1068 4 US-09-170-496D-1
40 205 12.9 1438 4 US-09-016-434-1426
41 204 12.8 1020 4 US-09-170-496D-31
42 203.5 12.8 1244 1 US-07-816-283-7
43 203.5 12.8 1244 1 US-08-417-103-7
44 203.5 12.8 1640 3 US-08-781-250-1
45 203 12.8 1236 4 US-09-016-434-717

AUTHORS GRASP Consortium, Davidson, W.S., Koop, B.F. and
<http://web.uvic.ca/cbr/grasp>.
TITLE A survey of Salmo salar transcripts from high complexity cDNA
 libraries
JOURNAL Unpublished (2002)
COMMENT Contact: Koop BF
 Centre for Biomedical Research
 University of Victoria
 PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
 Tel: 250 472 4067
 Fax: 250 472 4075
 Email: bkoop@uvic.ca
 Genome Sciences Centre, BC Cancer Agency cDNA preparation,
 sequencing and bioinformatics. Y Butterfield, R Kirkpatrick, J
 Asano, N Ginn, R Guin, D Lee, S Lee, T Olson, P Pandoh, A Prabhu, D
 Smailius, L Spence, J Scott, G Taylor, G Yang, J Schein, S Jones and
 M Marra.

FEATURES Location/Qualifiers
 source 1..648
 /organism="Salmo salar"
 /mol_type="mRNA"
 /strain="McConnell"
 /db_xref="taxon:8030"
 /clone_lib="mixed tissue"
 /note="vector: pCMVSPORT6; Library Creator: Research
 Genetics; Atlantic salmon tissue contributors: Carlo
 Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.),
 Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery
 (Crofton, B.C.), Rachel Roper (University of Victoria)"

ORIGIN

Alignment Scores:					
Pred. No.:	5.82e-18	Length:	648		
Score:	261.00	Matches:	51		
Percent Similarity:	59.84%	Conservative:	25		
Best Local Similarity:	40.16%	Mismatches:	31		
Query Match:	16.39%	Indels:	20		
DB:	14	Gaps:	2		

US-10-055-106C-2 (1-305) x CB514250 (1-648)

Qy	178	VallysrlelleantyrMetilleVallePheValleAlaValleAlaValleLeu	197
Db	616	GTCAAGTGTCTGAACACTACATCATGCTGTGTGATCATCATTTGGCCTGTGTGCTGACG	557
Qy	198	ValPheGlnValPheilleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSer	217
Db	556	GCACCTGCAGTGTCTATGTCATGCTCTTCTGCACAGGAAGTATGGCGGAGACTGCATGCT	497
Qy	218	HisGlnGluPheTrpAlaGlnLeuLysAsnLeuPhePheilleGlyValleLeuValCys	237
Db	496	CACCAGAGTCTGGGCTCAGCTGACGAGAGCTGTGTTTGGTGGTGTGTGTGTGTGT	437
Qy	238	PheLeuProTyrGlnPhePheArgileTyrTyrLeuAsnValValThrHisSerAsnAla	257
Db	436	TTTGTCCCTATACACGTTTCAGGATGTACTCTCTGGACACCTGTACTCTGGAGACACT	377
Qy	258	CysAsnSerLysValAlaPheTyrAsnGluillePheLeuSerValThrAlaIleSerCys	277
Db	376	-----AACGAGGTATTCTCTCATGCTCTCAGCGCCCTCAGCTGT	341
Qy	278	TyrAspLeuLeuLeuPheValPheGlyGlySerHisTrpPheLysGlnLysilleGly	297
Db	340	TTTCACATGCTTACTCTTC-----CTAGGG	317
Qy	298	LeuTrpAsnCysValLeuCys	304
Db	316	AGGGGACACTGCTATATGTGT	296

Search completed: April 25, 2004, 22:16:30
 Job time : 2909 secs

polyA+ RNA from equine peripheral blood leukocytes isolated from a healthy adult horse. The leukocytes were stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CATGTGTG, 3-prime DraIII site is CACCATGG). XhoI excises the cDNA insert."

ORIGIN

Alignment Scores:
Pred. No.: 3,16e-25 Length: 679
Score: 328.00 Matches: 66
Percent Similarity: 63.74% Conservative: 50
Best Local Similarity: 36.26% Mismatches: 62
Query Match: 20.60% Indels: 4
DB: 14 Gaps: 3

US-10-055-106C-2 (1-305) x CD469227 (1-679)

Qy 109 lLeuValThrArgTyrLeuIlePhePheLysCysLysAspLysValGluPheTyrArg 128
Db 2 ATTGTCATATCCGATTGCTCATCTATTATTAG---AACTCCCACTGCACAGTTAAAA 58
Qy 129 LysLeuHisAlaValAlaAlaSerAlaGlyMetThrThrLeuValIleValValVal 148
Db 59 AAGTACCATCGCGTATGTTTAAAGCATTTATTGATAGTGGGTAGCTTATTTTGTG 118
Qy 149 ProLeuValValSerArgTyrGlyIleHisGluGluTyrAsnGlu---GluHisCysPhe 167
Db 119 CCAATATTTCTTACTATATGGCAAGTACAGTCAAGTTACTCAGAACACAGATGCTTT 178
Qy 168 LysPheHisLysGluLeuAlaTyrThrTyrValLysIleIleAsnTyrMetIleValIle 187
Db 179 GAGTTCTCAAAAGACTTCAACACACAGGGAATTCATCTTGAATTTACTCTATGATGCC 238
Qy 188 PheValIleAlaValAlaValIleLeuValPheGlnValPheIleIleMetLeuMet 207
Db 239 ATTATGATGACAGTGGTGGTACCCCTCTTCTGATACAGATGGGTGTCATTTGCAACTC 298
Qy 208 ValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTyrAlaGlnLeuLysAsn 227
Db 299 ATAAAGGTTCTTTGGCCCTGACCTGCTGCTCATCAAGAGTATAGAGCTCAAAATCAAGAGC 358
Qy 228 LeuPhePheIleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIleTyr 247
Db 359 TGCCTTCTCTTCTAGTATAGTCGTCTGTTTATACCCCACTGATGCTTCCGGGTACAC 418
Qy 248 TyrLeuAsnValValThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsnGlu 267
Db 419 TTTCTTCAG-----AATATTCAGAGGAGAGAAATCTGAGTAGTCTTTTAAATGAA 472
Qy 268 lIlePheLeuSerValThrAlaIleSerCysTyrAspLeuLeuLeuPheValPheGlyGly 287
Db 473 ATTTTGTGGCTTAACTACTGCTGTGTCCTGGATAGCTGTGTTCTGAGTGGAGTT 532
Qy 288 SerHis 289
Db 533 ATCCAT 538

RESULT 12
LOCUS CD699779 499 bp mRNA linear EST 25-JUN-2003
DEFINITION EST16303 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD699779
VERSION CD699779.1 GI:32229387
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 499)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.

TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
source

1. 499
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Alignment Scores:
Pred. No.: 7.04e-24 Length: 499
Score: 314.00 Matches: 63
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.72% Indels: 0
DB: 14 Gaps: 0

US-10-055-106C-2 (1-305) x CD699779 (1-499)

Qy 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 20
Db 311 ATGCTGGCCACCAATACCTCCAGGAATTCCTCTGGCATCTATAGTACACCCACTTA 370
Qy 21 lIleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 40
Db 371 ATAGCCTTACTTCACTAGTCTTATGGCGGCTGGTGGTGTCTATTCATTCCTTTTC 430
Qy 41 LeuLeuValLysMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
Db 431 CTCCTGGTGAATGAACACCCCGTCAGTCACCATCGCGTCAATTAACTTGGTGGTG 490
Qy 61 ValHisSer 63
Db 491 GTCCACAGC 499

RESULT 13

LOCUS BG145683 478 bp mRNA linear EST 01-FEB-2001
DEFINITION mac33c07.y1 Soares mouse 3N3MS Mus musculus cDNA clone
IMAGE:4001652 5', mRNA sequence.

ACCESSION BG145683
VERSION BG145683.1 GI:12649019
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 478)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapss-f@mail.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1499380

Seq primer: -40RP from Gibco
High quality sequence stop: 392.
Location/Qualifiers
1. 478
/organism="Mus musculus"


```

Qy 218 sGlnGluphPheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPh 238
Db 672 TCAAGAGTCTTGCGCACACCTGAAGAATGTGTCTTCCTGGTATGTTTGTGTTT 731
Qy 238 eLeuProTyrGlnPhePheArgIleTyr 247
Db 732 TGTGCCCTATCAGGATTCAGAGTGAT 759

RESULT 8
AJ455645      834 bp mRNA linear EST 22-APR-2002
LOCUS      AJ455645
DEFINITION      riken1 Gallus gallus cdna clone 6b4r1, mRNA sequence.
ACCESSION      AJ455645
VERSION      AJ455645.1 GI:20265741
KEYWORDS      EST
SOURCE      Gallus gallus (chicken)
ORGANISM      Gallus gallus
REFERENCE      1 (bases 1 to 834)
AUTHORS      Buerstedde J.M.
TITLES      Gallus gallus bursal lymphocyte EST
JOURNAL      Unpublished (2002)
COMMENT      Contact: Buerstedde JM
              Cellular Immunology
              Heinrich-Pette-Institute
              Martinistr. 52, 20251 Hamburg, Germany
              Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES
    source
    1..834
        /organism="Gallus gallus"
        /mol_type="mRNA"
        /db_xref="taxon:9031"
        /clone="6b4r1"
        /cell_type="bursal lymphocyte"
        /dev_stage="2-3 weeks old"
        /clone_lib="riken1"
        /note="CB inbred strain"

ORIGIN
Alignment Scores:
Pred. No.:      1,43e-29      Length:      834
Score:      369.00      Matches:      72
Percent Similarity:      76.72%      Conservative:      17
Best Local Similarity:      62.07%      Mismatches:      26
Query Match:      23.18%      Indels:      1
DB:      9      Gaps:      0

US-10-055-106C-2 (1-305) x AJ455645 (1-834)

Qy 20 LeuIleSerLeuTyrPheIleValLeuIleGlyLeuValGlyValIleSerIleLeu 39
Db 439 CTGATTACTGTCTACTCAGTTGCGCTTTGCTGGAGGTGGATGATCCATCGCAATGTCA 498
Qy 40 PheLeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuVal 59
Db 499 TTGTGTGTGTCTCAGATGAACAGTCTGTCTGTGACCACTACAGCCAAATTAATCTAGTT 558
Qy 60 ValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLys 79
Db 559 GTGGTACATGGTCTCTCTCTCCACAGTGCCTTCGGTCTGCACTACTATGTCAAATAAG 618
Qy 80 ThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMet 99
Db 619 GAGTGGATCTTCCACATACCAATCTGTGTAATGTGTGAGTGTGATGGTGACATCCACATG 678
Qy 100 TyrLeuThrPheLeuPheTyrValIleLeuValThrArgTyrLeu-IlePhePhe 119
Db 679 TATTGATCTTCTTACTTCTAGCTGATCAGTGTGTGATCCGGNGGNTGGGCTTCTTTCA 738
Qy 119 sCysLysAspLysValGluPheTyrArgLysLeuHisAlaValala 134

```

```

Db 739 ATGGAAGGACACGGTAGAGTTTATAGAAAGCTNCATGCCATTGCT 784

RESULT 9
CA355790      680 bp mRNA linear EST 05-NOV-2002
LOCUS      CA355790
DEFINITION      627748 NCCWA 1RT Oncorhynchus mykiss cdna clone 1RT8K09_A_F05 5', mRNA sequence.
ACCESSION      CA355790
VERSION      CA355790.1 GI:24600977
KEYWORDS      EST.
SOURCE      Oncorhynchus mykiss (rainbow trout)
ORGANISM      Oncorhynchus mykiss
REFERENCE      1 (bases 1 to 680)
AUTHORS      Rexroad,C.E. and Keefe,J.W.
TITLES      Sequence analysis of a rainbow trout normalized cdna library
JOURNAL      Unpublished (2002)
COMMENT      Contact: Rexroad CE
              USDA, ARS, National Center for Cool and Cold Water Aquaculture
              11876 Leetown Road, Kearneysville, WV 25430, USA
              Tel: 304 724 8340 x2129
              Fax: 304 725 0351
              Email: crexroad@nccwa.ars.usda.gov
              Single pass sequencing. Bases called with phred v0.020425.c and
              trimmed with the aid of the trim_alt option. Vector identified by
              cross_match v0.990329.
              Seq primer: AGCGGATAACAATTTTCACACAGGA.

FEATURES
    Location/Qualifiers
    1..680
        /organism="Oncorhynchus mykiss"
        /mol_type="mRNA"
        /db_xref="taxon:8022"
        /clone="1RT8K09_A_F05"
        /tissue_type="pooled"
        /lab_host="DH10B"
        /clone_lib="NCCWA 1RT"
        /note="Vector: PCMV SPORF6; Site 1: NotI; Site 2: SalI;
              Library made from pooled tissue from brain, gill, liver,
              spleen, muscle, and kidney."

ORIGIN
Alignment Scores:
Pred. No.:      1,24e-29      Length:      680
Score:      368.50      Matches:      69
Percent Similarity:      69.28%      Conservative:      37
Best Local Similarity:      45.10%      Mismatches:      44
Query Match:      23.15%      Indels:      3
DB:      14      Gaps:      2

US-10-055-106C-2 (1-305) x CA355790 (1-680)

Qy 9 AnSerSerCysAspProIleValThrProHisLeuIleSerLeuTyrPheIleValLeu 28
Db 223 AACTCTACCATCTCCGACCTCAACGCTCTTACCCTGTGTTCATATAGCTGTGCTCG 282
Qy 29 IleGlyGlyLeuValGlyValIleSerIleLeuPheLeuValLysMetAsnThrArg 48
Db 283 GTCATTGGGGTCATCGGG---TTGGCCCTGATGATCCACATCTCCATCCACATGCGA 339
Qy 49 SerValThrThrMetAlaValIleAsnLeuValValHisSerValPheLeuLeuThr 68
Db 340 TCAGTTATCACCATCGCTATGCTCAACCTCACCTCGGCCCACTTCTGTTCTTACTCACC 399
Qy 69 ValProPheArgLeuThrTyrLeuIleLysLysThrTrpMetPheGlyLeuProPheCys 88
Db 400 GRACCCCTTCAGGATCTACTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459
Qy 89 LysPheValSerAlaMetLeuHisIleHisMetTyrLeuThrPheLeuPheTyrValVal 108
Db 460 AAGNGGTCAGTGCCCATGATCCACGTCGACATGATACGCTTTGTTTCTTACGCTGTC 519

```

/clone="IMAGE:4917024"
 /tissue type="tumor, gross tissue"
 /dev stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Mam4"

/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Priscilla Furth,
 NIH Reference for transgenic model; Li et al., Cell Growth
 and Differentiation 7, 3-11 (1996)."

ORIGIN

Alignment Scores:
 Pred. No.: 2,53e-43 Length: 646
 Score: 494.00 Matches: 97
 Percent Similarity: 90.27% Conservative: 5
 Best Local Similarity: 85.84% Mismatches: 11
 Query Match: 31.03% Indels: 0
 DB: 12 Gaps: 0

US-10-055-106c-2 (1-305) x BG862323 (1-646)

QY 1 MetProGlyHisAsnThrSerArgAsnSerCysAspProIleValThrProHisLeu 20
 DB 307 ATGGATGGATATAATACCTCTGAGATTCTCTGTGACCTATATCTGGCACCACTTA 366
 QY 21 IleSerLeuTyrPheIleValleuIleGlyLeuValGlyValIleSerIleLeuPhe 40
 DB 367 ACATCGATTACTTCATATGCTATGGAGACTGGTAGGCCCTCATCTCCATCCGGTTC 426
 QY 41 LeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuValVal 60
 DB 427 TTGCTGGTGAATGAATCACTCAGTTCAGTGACCACTGCTGTATCAACCTCGTGTG 486
 QY 61 ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleIleValThr 80
 DB 487 GTTCATGGGGTCTCTCTACTGACGGTGGCTTCCGCTTGGCATCTCATCAAGGGACT 546
 QY 81 TrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyr 100
 DB 547 TGGACGTTTGGATTACCTCTTGCAATTTGTGAGTGCCATGTTACATATCCACATGTAC 606
 QY 101 LeuThrPheLeuPheTyrValValIleLeuValThrArg 113
 DB 607 CTCACGTTCTCTTCTACGTGGTGATCATGTATCATCAGA 645

RESULT 7

CA965628 844 bp mRNA linear EST 03-JAN-2003
 CcLX05a15h17f1 Carp mixed tissue library 2 Cyprinus carpio cDNA
 clone 15h17 5', mRNA sequence.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

CA965628.1 GI:27492185

EST.

Vector has been trimmed from this EST.

Plate: 15 row: h column: 17

Seq primer: TripleX 5' LD (5'-CTCGGGAAGCGCGCATTTGTTGGT-3')

High quality sequence start: 39

High quality sequence stop: 580.

FEATURES

Location/Qualifiers

1..844

/organism="Cyprinus carpio"

/mol_type="mRNA"

/db_xref="taxon:7962"

/clone="15h17"

/sex="Male & female"

/tissue_type="Skeletal white muscle, cardiac muscle,

kidney, brain, gill, intestinal mucosa"

/dev_stage="Adult"

/lab_host="E.coli Electromax DH10B"

/clone_lib="Carp mixed tissue library 2"

/notes="Vector: pTriplex2; Site 1: SfiI GGCCATTACGGCC;

Site 2: SfiI GGCGCTCGGC; Normalized and serially

subtracted cDNA library prepared from mixed tissues of

warm, cold and hypoxia challenged animals"

ORIGIN

Alignment Scores:

Pred. No.: 3.37e-39 Length: 844

Score: 457.50 Matches: 92

Percent Similarity: 60.43% Conservative: 47

Best Local Similarity: 40.00% Mismatches: 87

Query Match: 28.74% Indels: 4

DB: 14 Gaps: 3

US-10-055-106c-2 (1-305) x CA965628 (1-844)

QY 20 LeuIleSerLeuTyrPheIleValleuValleuValGlyValIleSerIleLeu 39
 DB 78 CTTCGTGTTGTAATATATTCATCTTCTTGTGGGGACTCTGAATGTTGTAATAATGCC 137
 QY 40 PheLeuLeuValIleMetAsnThrArgSerValThrMetAlaValIleAsnLeuVal 59
 DB 138 TGTATGTACAGTCCCAAGGGCGTCTCTTCCACCAAGGTCTGTATATCAACCTGATA 197
 QY 60 ValValHisSerVal-PheLeuLeuThrValProPheArgLeuThrTyrLeuIle---Ly 78
 DB 198 GCAGTGCATCCCTTTCTCTCAGGTGGCCCTTCGATTACTATTATGCTTCTAA 257
 QY 78 sLysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHi 98
 DB 258 TAAAGACTGGATTCTTGGCATACATTTCTGCAAAATTTGTCAGTATATATGATCCCA 317
 QY 98 sMetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIlePhePh 118
 DB 318 CATGTATCTTGCATTTATCTTCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 377
 QY 118 eLysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAalaSerAlaGl 138
 DB 378 TGATCAACAACAACAGCTAAAGTTTCATCGCATCTTCACGCCACGATTGCAAGTCAAG 437
 QY 138 yMetTrpThrLeuValIleValIleValProLeuValValSerArgTyrGlyIleHi 158
 DB 438 CGTCTGGATGTCATATTCGGTGTATGATGCCA---GCACTGCTAATATGGAATGGC 494
 QY 158 sGluGluTyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrVa 178
 DB 495 ACAGAAC---GATTCAACTCATTTGTTTAAATTTTGGTCAGGCTCTCACCCAGCTACTGT 551
 QY 178 lLysIleIleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuVal 198
 DB 552 GAAACATTAACATCTATTAATTTGTACTANTAACTACTGTTTGGAGTGTCTTGGCAGT 611
 QY 198 lPheGlnValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuSerHi 218
 DB 612 TTTCAGATTATTTTCTGCTCAAGTGAAGTAAACATTTTGGAAAGGCCACATGTCAACG 671

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-xes@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

source

1. 2774
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:A530099J19"
/db_xref="MGI:2406345"
/db_xref="taxon:10090"
/clone="A530099J19"
/sex="male"
/tissue_type="aorta and vein"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
311..1210
/notes="unnamed protein product; hypothetical
Rhodopsin-like GPCR superfamily containing protein
(InterPro:IPR00276, evidence: InterPro)
putative"

CDS

/codon_start=1
/protein_id="BAG30904.1"
/db_xref="GI:26334373"
/translation="MDVMDVLDVNSGVVPMQVCDHCAILTYAVSVFQGT
VGVVMHMYLTIFFYVAIVTLRLIYFKLQOOLQKPHAVALSIIWVTSFIFLP
LIFQVGTDPSTYEQRCFPHKLSNRDIIINYSTIVIMTIVLLFLIQMAVILH
LIKAYMDMAHQBRYRAQIKSPFFLLIVVCFIPHAFRVYFIQNPQENSKLLIYN
EICVALTAFCLDMLCFIGVH"

ORIGIN

Alignment Scores:
Pred. No.: 2,45e-47 Length: 2774
Score: 538.50 Matches: 105
Percent Similarity: 58.97% Conservative: 66
Best Local Similarity: 36.21% Mismatches: 106
Query Match: 33.83% Indels: 13
DB: 11 Gaps: 4

US-10-055-106C-2 (1-305) x AK041317 (1-2774)

QY 12 CysAspProIleValThrProHisLeuIleSerLeuTyrPheIleValLeuIleGly 31
Db 380 TGTGATGCTCACTCAGACGAATTCGACACACCTATAGTGCGCTTCTTTGGAGGC 439
QY 32 LeuValGlyValIleSerIleLeuPheLeuValIleMetAnThrArgSerValThr 51
Db 440 ACCGTTGGACAGTATGATGTCACATGATGTTCAAGAGGAATGCCAATCAATGATT 499
QY 52 ThrMetAlaValIleAsnLeuValValHisSerValPheLeuThrValProPhe 71
Db 500 GCCACTATCATATATATCATGTGTGACCTCCCTTCTCTGATAGTATGCCATTC 559
QY 72 ArgLeuThrTyrLeuIleLysLeuThrTrpMetPheGlyLeuProPheCysLysPheVal 91
Db 560 CGGCTCAGTTACTATTTCTCAGCAGCTCGAAGCTGGGTCTTTTACCTGCCGAATGTT 619
QY 92 SerAlaMetLeuHisIleHisMetTyrLeuThrPheLeuPheTyrValValIleLeuVal 111
Db 620 AGTGGCGTCATATATGTCATATGATACCTTACCTTCAATTTTATGTCGCAATGTACC 679
QY 112 ThrArgTyrLeuIlePhePheLysCysLysAspLysValGluPheTyrArgLysLeuHis 131

Db 680 CTTCCGGCTGCATCATCTATTTTAAG---AACTGCAATGCAACAGTACAAAGTTCAT 736
QY 132 AlaValAlaAlaSerAlaGlyMetTrpThrLeuValIleValIleValValProLeuVal 151
Db 737 GCGGTGGCTCTAAGTATTATTATTGGGTGACAGAGCTTCATCTTTTACCATAATTT 796
QY 152 ValSerArgTyrGlyIleHisGluGluTyrAsnGlu---GluHisCysPheLysPheHis 170
Db 797 TTTTACAAATATGGCAGATCCAGATTATACAGACCAACGCGTGTCTTGATTTTCAT 856
QY 171 LysGluLeuAlaTyrThrTyrValLysIleLeuAsnTyrMetIleValIlePheValIle 190
Db 857 AAATCTCTCAATCCAGGACATCATCAATAAATCTATAAATGTTATTATGATG 916
QY 191 AlaValAlaValIleLeuValPheGlnValPheIleIleMetLeuMetValGlnLys 210
Db 917 ACAACAGTTCTGCTCTCTTTCTGATACAGATGGTGTCTATCTTCATTTATAAGCC 976
QY 211 LeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsnLeuPhePhe 230
Db 977 TATTGGCTGATATGTGGCCCATCAAGATACAGAGCTCAATCAACAGATTTTCTTC 1036
QY 231 IleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIleTyrTyrLeuAsn 250
Db 1037 CTGTGGTCATATGTCTCTTTATACCCACCATTCATTCAGGATATATTTATTCAA 1096
QY 251 ValValThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsnGluIlePheLeu 270
Db 1097 AATTTCCAGACCAAGAA-----AATCTAAGTTAATCTGTACAAATGAATCTGTGT 1150
QY 271 SerValThrAlaIleSerCysTyrAspLeuLeuPheValPheGlyGlySerHis--- 289
Db 1151 GCTTTAACAGCTTCTGCTGCTGATATGTTATGTTTCATAGGTGTGTCTCATCCATTAG 1210
QY 290 -----TTPhe 291
Db 1211 ACCTTCCCGTGTCTTCTGTGATTGGTTT 1240

RESULT 6
LOCUS BG862323 646 bp mRNA linear EST 29-MAY-2001
DEFINITION 602796201F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917024 5',
mRNA sequence.
ACCESSION BG862323
VERSION BG862323.1 GI:14212861
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 646)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0828 row: b column: 01
High quality sequence stop: 644.
Location/Qualifiers
1. 646
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
/db_xref="taxon:10090"

AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
TITLE Totoki, Y., Watanabe, H. and Sakaki, Y.
JOURNAL BAC end sequences of Library RPCI-43
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 684)
TITLE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
JOURNAL Totoki, Y., Watanabe, H. and Sakaki, Y.
REFERENCE Direct Submission
AUTHORS Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
TITLE and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
JOURNAL 1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
REFERENCE (E-mail: chimpsesgsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
AUTHORS Tel: 81-45-503-9111, Fax: 81-45-503-9170)
TITLE Clones are derived from the chimpanzee BAC library RPCI-43. This BAC
JOURNAL end was generated during the R&D process and may have higher chance
REFERENCE of clone tracking errors.
AUTHORS PRIMERS
TITLE Sequencing: TU
JOURNAL LIBRARY
REFERENCE Vector : pBAC3.6
AUTHORS R.Site 1 : EcoRI
TITLE R.Site 2 : EcoRI.
JOURNAL Location/Qualifiers
REFERENCE 1. 684
AUTHORS /organism="Pan troglodytes"
TITLE /mol_type="genomic DNA"
JOURNAL /db_xref="taxon:9598"
REFERENCE /clone="RP43-007G22.TU"
AUTHORS /sex="male"
TITLE /cell_type="lymphocytes"
JOURNAL /clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Alignment Scores:
 Pred. No.: 1.29e-91 Length: 684
 Score: 938.00 Matches: 179
 Percent Similarity: 96.76% Conservative: 0
 Best Local Similarity: 96.76% Mismatches: 6
 Query Match: 58.92% Indels: 0
 DB: 29 Gaps: 0

US-10-055-106C-2 (1-305) x AG145972 (1-684)

QY 121 LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaSerAlaGlyMetThr 140
 Db 10 AAAAATCCGCGCTTCTACAGAAATGTCATGCTGCTGCCAGTCTGCCATGCG 69
 QY 141 ThrLeuValLeuValLeuValProLeuValValSerArgTyrGlyHisGluGlu 160
 Db 70 ACGCTGTGTATTCATTTGGTACCCCTGGTGTCTCCCGGATGGAATCCATGAGAA 129
 QY 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180
 Db 130 TACAATGAGGAGGACGTGTTTACATTTACAAGAGCTTGCTTACACATATGTGAAATC 189
 QY 181 IleAsnTyrMetLeuValLeuPheValIleAlaValAlaValLeuLeuValPheGln 200
 Db 190 ATCAACTATATGATGATGATTTTGTTCATGCGCTGCTGCTGATTCGTGGTCCTCCAG 249
 QY 201 ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
 Db 250 GTCTTCATCATTAATGTTGATGGTGAGAGCTAGCCACTCTTTACTATCCACAGGAG 309
 QY 221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValLeuValCysPheLeuPro 240
 Db 310 TTCGGGCTCAGCTGAAACCACTATTTTATAGGGGTCTATCTGTTGTTTTCCTTCCC 369
 QY 241 TyrClnPhePheArgIleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
 Db 370 TACAGTTCCTTAGAATCTATTAATGATGTTGTGACGATTCCTAATGCTGTACAGC 429
 QY 261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280

Db 430 AAGTTGCATTTTATAACGAATCTTTGAGCTGTAAACAGCAATTAGCTGTATGATTG 489
 QY 281 LeuLeuPheValPheGlySerHisThrPheLysGlnLysIleIleGlyLeuThrPhe 300
 Db 490 CTTCTCTTTGCTTTGGGGAGCCATTCGTTTAAACAAAAGATTAATGACTTAAGGAAT 549
 QY 301 CysValLeuCysArg 305
 Db 550 TGAGTTTGTGCGGT 564

RESULT 2
 BF160725 772 bp mRNA linear EST 30-OCT-2000
 LOCUS 601769127F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3988230 5',
 DEFINITION mRNA sequence.
 ACCSSION BF160725
 VERSION BF160725.1 GI:11040832
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 772)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM9196 row: f column: 07
 High quality sequence stop: 634.
 Location/Qualifiers
 1. 772
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="taxon:10090"
 /clone="IMAGE:3988230"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 Stem Cell Origin.
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Lu29"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

ORIGIN

Alignment Scores:
 Pred. No.: 2.27e-81 Length: 772
 Score: 844.50 Matches: 177
 Percent Similarity: 88.02% Conservative: 14
 Best Local Similarity: 81.57% Mismatches: 25
 Query Match: 53.05% Indels: 3
 DB: 10 Gaps: 1

US-10-055-106C-2 (1-305) x BF160725 (1-772)

QY 31 GlyLeuValGlyValIleSerIleLeuPheLeuValLysMetAsnThrArgSerVal 50
 Db 1 GGACTGGTAGGCGCTCATCTCCATCTCTTCTTCTGTTGTTGAAATGAACTCAGTTCAGTG 60
 QY 51 ThrThrMetAlaValIleAsnLeuValValHisSerValPheLeuLeuThrValPro 70
 Db 61 ACCACCATGGCTGTATCAACCTGGTGGTGGTTCATGGGCTCTTCTACTACGGTGGCT 120
 QY 71 PheArgLeuThrTyrLeuIleLysLysThrTrpMetPheGlyLeuProPheCysLysPhe 90

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 25, 2004, 19:56:50 ; Search time 2904 Seconds
(without alignments)
3136.352 Million cell updates/sec

Title: US-10-055-106C-2
Perfect score: 1592
Sequence: 1 MPGHNTSRNSSCDPIVTPHL.....GGSHWFKQKIIGLWNCVLCR 305

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US10055106/runat_21042004_161131_26191/app_query.fasta_1.455
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR score=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10055106@cgn_1_1_2810 @runat_21042004_161131_26191 -NCPU=6 -ICPU=3
-NO MAP -LARGSEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	938	58.9	684	29	AG145972 Pan trogl
2	844.5	53.0	772	10	BF160725 601769127
3	704	44.2	580	28	A2554824 RPCI-23-2
4	574	36.1	456	28	AQ888495 HS 3162 B
5	538.5	33.8	2774	11	AQ041317 Mus muscu
6	494	31.0	646	12	BG862323 602796201
7	457.5	28.7	844	14	CA965628 CCLX05A15
8	369	23.2	834	9	AJ455645
9	368.5	23.1	680	14	CA355790 627748 NC
10	356	22.4	649	12	BG461295 RST44080
11	328	20.6	679	14	CD469227 LeukOS2_2
12	314	19.7	499	14	CD699779 EST16303
13	305	19.2	478	12	BG145683
14	288.5	18.1	733	13	CA050323
15	261	16.4	648	14	CB514250
16	249	15.6	283	12	BG221739 RST41554
17	241.5	15.2	2755	11	AK033476 Mus muscu
18	236.5	14.9	1081	29	AY406930 Pan trogl
19	236	14.8	1149	29	AY406931 Mus muscu
20	235	14.8	1856	11	AK039528 Mus muscu
21	231.5	14.5	1146	29	AY406929 Homo sapi
22	231.5	14.5	1199	11	AF345566 Homo sapi
23	229.5	14.4	1878	11	AK033675 Mus muscu
24	228	14.3	1819	11	AK039041 Mus muscu
25	225.5	14.2	1014	29	AY404081 Mus muscu
26	218	13.7	1176	29	AY400827 Homo sapi
27	218	13.7	1176	29	AY400829 Mus muscu
28	218	13.7	2014	11	AK046464 Mus muscu
29	217	13.6	1002	29	AY406923 Homo sapi
30	217	13.6	1258	11	AF345567 Homo sapi
31	217	13.6	1990	11	BC040850 Homo sapi
32	217	13.6	2938	11	BC045651 Homo sapi
33	215	13.5	936	29	AY401365 Homo sapi
34	215	13.5	996	29	AY401366 Pan trogl
35	214.5	13.5	1501	11	AK080394 Mus muscu
36	214	13.4	834	29	CS586141 CH240_383
37	211.5	13.3	996	29	AY401367 Mus muscu
38	211	13.3	1062	29	AY400424 Mus muscu
39	210.5	13.2	1687	11	AK039791 Mus muscu
40	210	13.2	987	29	AY401371 Homo sapi
41	210	13.2	2724	11	BC033445 Homo sapi
42	208.5	13.1	1008	29	AY406925 Mus muscu
43	208	13.1	2708	11	AK076275 Mus muscu
44	207.5	13.0	814	29	AY405237 Homo sapi
45	207.5	13.0	960	29	AY409037 Mus muscu

ALIGNMENTS

RESULT 1
AG145972
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey
684 bp DNA linear GSS 08-JAN-2002
ACCESSION AG145972
VERSION AG145972.1 GI:16675650
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1